WEST Search History

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DATE: Monday, June 21, 2004

Hide?	<u>Set</u> Name	Query	<u>Hit</u> Count
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	L17	L16 same 12	2
	L16	catalytic adj domain	2478
	L15	L14 not 13	2
	L14	12 same 113	4
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	L8	12 near20 L7	0
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	L4	james.in.	203604
	L3	11 and L2	3
	L2	starch adj (synthase or synthetase)	197
	L1	myers.in.	5098

END OF SEARCH HISTORY

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Generate OACS

Search Results - Record(s) 1 through 3 of 3 returned.

☐ 1. Document ID: US 6639125 B1

L3: Entry 1 of 3

File: USPT

Oct 28, 2003

US-PAT-NO: 6639125

DOCUMENT-IDENTIFIER: US 6639125 B1

TITLE: Dull1 coding for a starch synthase and uses thereof

Full Title Citation Front Review Classification Date Reference Cla

□ 2. Document ID. US 0410/10 B.

L3: Entry 2 of 3

File: USPT

Jun 25, 2002

US-PAT-NO: 6410716

DOCUMENT-IDENTIFIER: US 6410716 B1

TITLE: Isolation of SU1, a starch debranching enzyme, the product of the maize gene

sugaryl

Full Title Citation Front Review Classification Date Reference State State Claims KWC Draw De

☐ 3. Document ID: US 5981728 A

L3: Entry 3 of 3

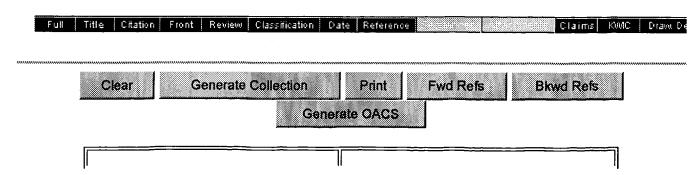
File: USPT

Nov 9, 1999

US-PAT-NO: 5981728

DOCUMENT-IDENTIFIER: US 5981728 A

TITLE: Dull1 coding for a novel starch synthase and uses thereof



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Search Results - Record(s) 1 through 7 of 7 returned.

☐ 1. Document ID: US 6391551 B1

L6: Entry 1 of 7

File: USPT

May 21, 2002

US-PAT-NO: 6391551

DOCUMENT-IDENTIFIER: US 6391551 B1

TITLE: Detection of nucleic acid hybrids

US-PAT-NO: 6350934

DOCUMENT-IDENTIFIER: US 6350934 B1

TITLE: Nucleic acid encoding delta-9 desaturase

Full Title Citation Front Review Classification Date Reference Claims RWC Draw Do

US-PAT-NO: 5675064

DOCUMENT-IDENTIFIER: US 5675064 A

TITLE: Starch and grain with a novel genotype

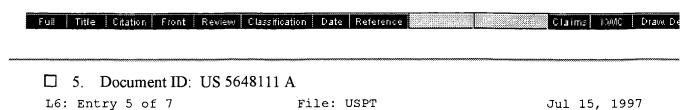
Full Title Citation Front Review Classification Date Reference Claims KWC Draw. De Cla

US-PAT-NO: 5648249

DOCUMENT-IDENTIFIER: US 5648249 A

Record List Display Page 2 of 3

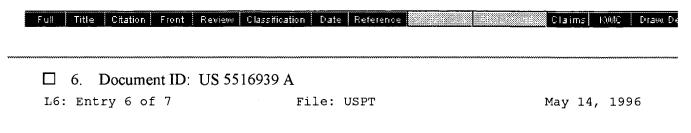
TITLE: Method of improving the quality of stored potatoes



US-PAT-NO: 5648111

DOCUMENT-IDENTIFIER: US 5648111 A

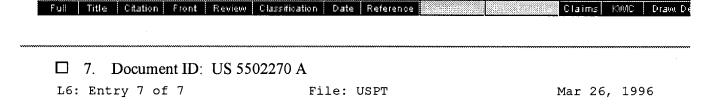
TITLE: Starch and grain with a novel genotype



US-PAT-NO: 5516939

DOCUMENT-IDENTIFIER: US 5516939 A

TITLE: Starch and grain with a novel genotype

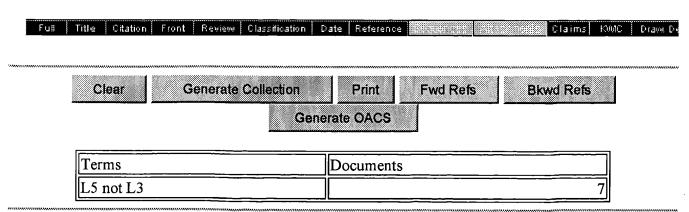


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DOCUMENT-IDENTIFIER: US 5502270 A

** See image for Certificate of Correction **

TITLE: Starch and grain with a novel genotype



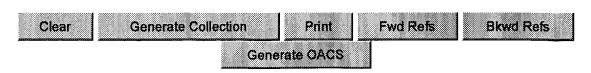
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☐ 1. Document ID: US 6642437 B1

L12: Entry 1 of 3

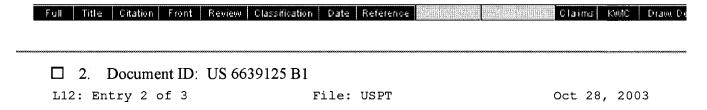
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Nov 4, 2003

US-PAT-NO: 6642437

DOCUMENT-IDENTIFIER: US 6642437 B1

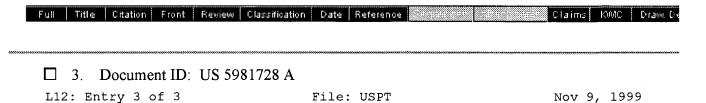
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US-PAT-NO: 6639125

DOCUMENT-IDENTIFIER: US 6639125 B1

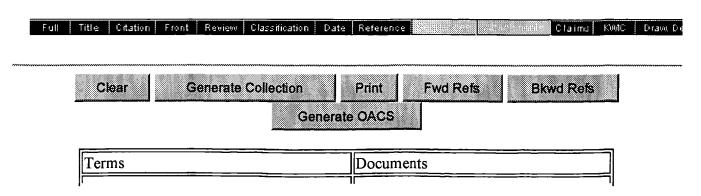
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DOCUMENT-IDENTIFIER: US 5981728 A

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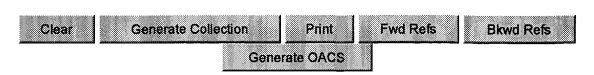


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Display Format: TI Change Format

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L15: Entry 1 of 2

File: USPT

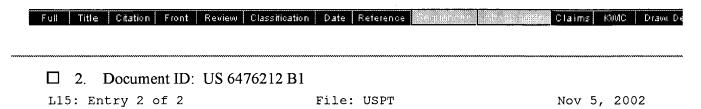
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TITLE: Nucleic acid molecules from plants encoding enzymes which participate in

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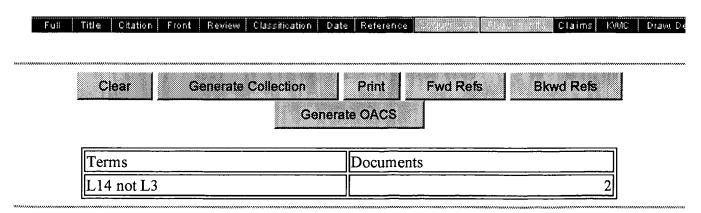


US-PAT-NO: 6476212

DOCUMENT-IDENTIFIER: US 6476212 B1

** See image for Certificate of Correction **

TITLE: Polynucleotides and polypeptides derived from corn ear





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     Chimeric genes and starch synthases with heterologous glucan-binding and
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     2002
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     An immunoenzymatic solid-phase assay for quantitative determination of
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     Corn starch synthase isoenzyme and cDNA, transgenic plants expressing this
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     Chain-length specificities of maize starch synthase I enzyme: Studies of
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     Fusion proteins with Chlamydomonas starch synthase and food and
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     The structure and expression of the wheat starch synthase III gene. Motifs
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     in the expressed gene define the lineage of the starch synthase III gene
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family

2000

PΥ

- L7 ANSWER 7 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 4
- TI Expression of a cassava granule-bound starch synthase gene in the amylose-free potato only partially restores amylose content
- PY 1999
- L7 ANSWER 8 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 5
- TI Specificity of starch synthase isoforms from potato
- PY 1999
- L7 ANSWER 9 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 6
- TI Identification of the soluble starch synthase activities of maize endosperm
- PY 1999
- L7 ANSWER 10 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 7
- TI Isolation and characterization of the zSSIIa and zSSIIb starch synthase cDNA clones from maize endosperm
- PY 1998
- => d 17 ab 5-10
- => d 17 7 bib
- L7 ANSWER 7 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 4
- AN 132:247052 CA
- TI Expression of a cassava granule-bound starch synthase gene in the amylose-free potato only partially restores amylose content
- AU Salehuzzaman, Shah N. I. M.; Vincken, Jean-Paul; Van De Wal, Marion; Straatman-Engelen, Irma; Jacobsen, Evert; Visser, Richard G. F.
- CS The Graduate School Experimental Plant Sciences, Laboratory of Plant Breeding, Wageningen Agricultural University, Wageningen, 6700 AJ, Neth.
- SO Plant, Cell and Environment (1999), 22(10), 1311-1318 CODEN: PLCEDV; ISSN: 0140-7791
- PB Blackwell Science Ltd.
- DT Journal
- LA English
- => d 17 9 bib
- L7 ANSWER 9 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 6
- AN 131:99886 CA
- TI Identification of the soluble starch synthase activities of maize endosperm
- AU Cao, Heping; Imparl-Radosevich, Jennifer; Guan, Hanping; Keeling, Peter L.; James, Martha G.; Myers, Alan M.
- CS Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State University, Ames, IA, 50011, USA
- SO Plant Physiology (1999), 120(1), 205-215 CODEN: PLPHAY; ISSN: 0032-0889
- PB American Society of Plant Physiologists
- DT Journal
- LA English
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     Cao, Heping; James, Martha G.; ***Myers, Alan M.***
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     WO 9924575 A1 19990520 WO 1998-US24225 19981112
US 5981728 A 19991109 US 1997-968542
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AU 9915236 A1 19990531 AU 1999-15236 19981112
AU 761419 B2 20030605
EP 1030922 A1 20000830 EP 1998-959440 19981112
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MX 200004586 A 20001110 MX 2000-4586 20000512
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US 6639125 B1 20031028
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```

ANSWER 4 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN L11 AN ' 2000:278998 BIOSIS PREV200000278998 DN Dull1 coding for a novel ***starch*** ***synthase*** and uses TIthereof. ***Myers, Alan M.*** [Inventor, Reprint author]; James, Martha G. ΑU [Inventor] Des Moines, IA, USA CS ASSIGNEE: Iowa State University Research Foundation, Inc., Ames, IA, USA US 5981728 November 09, 1999 PIANSWER 5 OF 9 CA COPYRIGHT 2004 ACS on STN DUPLICATE 3 L11 131:99886 CA ANIdentification of the soluble TIactivities of maize endosperm Cao, Heping; Imparl-Radosevich, Jennifer; Guan, Hanping; Keeling, Peter AU L.; James, Martha G.; ***Myers, Alan M.*** Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State CS University, Ames, IA, 50011, USA Plant Physiology (1999), 120(1), 205-215 SO CODEN: PLPHAY; ISSN: 0032-0889 American Society of Plant Physiologists PB DTJournal English LAANSWER 6 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN L112003:144471 BIOSIS AN PREV200300144471 DNIdentification and characterization of the ***starch*** ΤI ***synthase*** activity coded for by maize gene dull1. Cao, Heping [Reprint Author]; ***Myers, Alan M.***; James, Martha G. ΑU Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State CS University, Ames, IA, USA hpcao@iastate.edu Plant Biology (Rockville), (1999) Vol. 1999, pp. 193. print. SO Meeting Info.: Annual Meeting of the American Society of Plant Physiologists. Baltimore, Maryland, USA. July 24-28, 1999. American Society of Plant Physiologists (ASPP). DTConference; (Meeting) Conference; (Meeting Poster)
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Identification of DU1 protein as a major soluble ***starch***

PREV200300119968

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     Plant Biology (Rockville), (1998) Vol. 1998, pp. 119. print.
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ΑU
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     G. [Reprint Author];
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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e 16027 /organism="unknown" /mol_type="unassigned DNA"	/ Match Local Similarity 100.0%; Score 2598; DB 6; Length 6027; Local Similarity 100.0%; Pred. No. 0; nes 2599; ¿Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 AGCTTGCTGAAAAATTATTGGCTGGGAAACAAGTTGTTTACTTATCCAGATGTATTGA 60 	61 AAGCTGATTCAACAATTGATCTCTATTTCAATGGTGATCTATCAGCTGTGGCCAATGAGC 120 	121 CTGATGTACTTATCAAAGGAGCATTCAATGGGTGGAAGTGGAGGATTTTTCACTGAAAAAT 180 	181 TGCACAAGAGCGAGCTGGCAGGGACTGGTGGTGCTGCAAACTATACATTCCTAAGCAGG 240 	241 CATACAGAATGGACTTTGTGTTTTTAACGGACACACGGTATATGAAAATAATAACAATA 300 2665 CATACAGAATGGACTTTGTGTTTTTTAACGGACACACGGTATATGAAATAATAACAATA 2724	301 AIGAITICGIGAIACAAAIAGAAAGCACCAIGGAAAAITIAITITAITIGAGAITITCTIGG 360 	361 CTGAAGAAAGGAAGGAGAACTTGAAAACTTGGAAATGAGGAAGCTGAAAGGAGGAGGA 420 	421 AAACTGATGAGCAGCGGAATGGAGGAAGAAGAAGGGCCGCAGATAAAGCTGACAGGTAC 480 	481 AAGCCAAGGTTGAGGTAGAGGACGAAGAATAAATTGTGCAATGTATTGGGTTTAGGCA 540 2905 AAGCCAAGGTTGAGGTAGAGACGAAGAAGAATAAATTGTGCAATGTATTGGGTTTAGCCA 2964	541 GAGCTCCTGTTGATAATTTATGGTACATTGAGCCCATCACGACTGGACAAGAGGCTACTG 600 1965 GAGCTCCTGTTGATAATTTATGGTACATTGAGCCCATCACGACTGGACAGAGAGACTACTG 3024	601 TCAGATTGTATTATAACATAAACTCAAGACCTCTAGTTCACAGTACTGAGATATGGATGC 660 3025 TCAGATTGTATTATAACATAAACTCAAGACCTCTAGTTCACAGTACTGAGATATGGATGC 3084	661 ATGGTGGCTATAACAATTGGATTGATGGACTCTCTTTTGCTGAAGGCTTGTTCATC 720 	721 AIGACAAAGATIGIGGATITGGGGGTITIGCAGAIGTIGICGGGCCIGAAAGAACATAIGIATA 780 	781 IGGACIGGGTITITGCIGACGGCCACCAGGGGAGTGCAAGGAATTATGACAACAAIGGAG 840 	841 GACATGATTTTCATGCTACCCTTCCAAATAACATGACTGAGGAAGAGTATTGGATGGA	901 aagaacaaaggatctatrcaaggcttcaacaagagaggaggagggagggggggggg
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REI 7	ORGANISM REFERENCE AUTHORS TITLE JOURNAL	Zea mays Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. 1 (bases 1 to 6021) Myers, A.M. and James, M.G. Myll coding for a novel starch synthase and uses thereof Patent: JP 2001552804-A 1 20-MOV-2001, Patent: JP 20-MOV-2001,
CO	COMMENT	10WA STATE UNITERSTITE EDEARCH FOUNTAINES OS Zea mays (maize) PN JP 2001522604-A/1 PD 20-NOV-2001 PF 12-NOV-1997 US 08/968542 PF 12-NOV-1997 US 08/968542
		ZN15/09,A01H5/00,C12 CDNA sequence cor synthase enzyme DU1. Key source
ਸ ਮ	FEATURES source	ri Location/Qualifiers 1. :6027 /organism="Zea mays" /mol_typ=="genomic DNA" /db_xref="taxon:4577"
OR	ORIGIN Query Match Best Local Matches 259	7 02 B
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Zea mays starch synthase DULL1 (dull1) mRNA, complete cds.
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( pases 1 to 6027)
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2 (bases 1 to 6027)
Gao, M., James, M.G. and Myers, A.M.
Direct Submitssion
Submitted (06-SEP-1997) Biochemistry & Biophysics, Iowa State
University, 2152 Molecular Biology Builiding, Ames, IA 50011, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gao, M., Wanat, J., Stinard, P.S., James, M.G. and Myers, A.M. Characterization of dull1, a maize gene coding for a novel starch
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be the maize starch synthase defined biochemically as
SSII"
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NALLSTETAEWTDNREAETAKADSSQNALSSSIIGEVDVADEDILAADLTVYSLSSVM
KKEVDAADKARVKEDAFELDLPATTLRSVIVDVMDHNGTVQETLRSVIVDVMDHNGTV
QETLRSVIVDVMDDAADKARVEEDVFELDLSGNISSSATTVELDAVDEVQDKFEA
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TSDSSGNVSTSARMOALIEPTVADDDPPEADLSGNASGGTYTREVDDVDDFTREBEDT
FAMDLFASEGGHEKHVAVDYVGEATDEEETYQQQYPVBSSFSWNDKALAKTGVSLNPE
IRLVRVBEQGKVNFSDKKDLSIDDLFQQNQSIIGSYKQDKSIADVAGPTQSIFGSSKQ
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VDRQDALYVNGLEAKEGDHTSRKTDEDALHVKFNVDNVIRKHQADRTQAVEKKTWKKV
DEEHLYMTEHQKRAAEGQMVVNEDELSITEIGMGRGDKIQHVLSBEELSWSEDEVQLI
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KRADSV1D1XINRDLTALANBEDVVTKGAFNGWRKLFPTEATHSKDLGGVWWSCKLY1
PKEAYRLDFVFFNGSTYYENNGNNDFC1G1EGTMNEDLFEDFUKEKQRELEKLAMEB
AERRTQTEEQRRRKEARAADEAVRAQAKAEIEIKKKKLQSMLSLAKTCVDNLWIIEAS
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VIPPEKALVLDWVFADGPAGNARNYDNNARQDFHAILPNNNVTEEGFWAQEEQNIYTR
LLQERREKEETWKRKAERSANIKAEMKAKTWRRFLLSQKHIVYTEPLEIRAGTTVDVL
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EPQNGMFGVGCVYGRNDDRRFGFFCHSALEFILQNEFSPHIIHCHDWSSAPVAMLYKE
HYSQSRMASTRVVFIIHNLEFGAHYIGKAMTYCDKATTVSPTYSRDVAGHGAIAPHRE
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FVFSEWEEDGIYDNRNGMDYHIPVSDSIETENYMRIHIAVEMAPVAKVGGLGDVVTS
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ITRLTAQKGIHLIKHAIHRTLESNGHVVLLGSAPDHRIQGDFCRLADALHGVYHGRVK
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DNDKDRARSLGLEPNGFSFDGADSNGVDYALNRAIGAWFDARDWFHSLCKRVMEQDWS
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Gale, K.R., Appels, R. and Morell, M.K.
The structure and expression of the wheat starch synthase III
Motifs in the expressed gene define the lineage of the starch
synthase III gene family
Plant Physiol. 123 (2), 613-624 (2000)
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Li,Z., Mouille,G., Kosar-Hashemi,B., Rahman,S., Clarke,B.,

Gale,K.R., Appels,R. and Morell,M.K.

Direct Submission

Submitted (19-APR-2000) CSIRO Division of Plant Industry,

1600, Canberra, ACT 2601, Australia

Location/Qualifiers
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/organism="Triticum aestivum"
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db_xref="G1:9502143"
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/db_xref="taxon:4565"
/chromosome="1"
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GAACATGIGITGATAATTTGIGGIACATAGAGGCTAGCACAGATACAAGAGGAGATACTA
                                                                                            CATACAGAATGGACTTTGTGTTTTTAACGGACACACGGTATATGAAAATAACAATA
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                                                                                                                                                         cchacadannagachringigirchrcaacdgrocacaddhahaadaadahagadaad
                                                                                                                                                                                                                      2493 ATGATTICTGTATAGGAATAGAAGGCACTATGAATGAAGATCTGTTTGAGGATTTCTTGG
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3453 CCTATATGATGATGTTTTCTCCGAGTGGGAAGAAGATGGGATCTATGACACAGGA 3512 1318 ATGGGTTAGACTATCATATTCTCTGTTTTTGGGTCAATTGCAAAGGAACCACCTATGCACA 1377 3513 ATGGGATGGATGCATATTCCTGTTTTCTGATTGAAACAGAGAATTACATGCGTA 3572 1378 TTGTCCACATTGCTGTTGATGCCCCAATCGCAAAGGTTGGAGGTCTTGGTGGTTG 1437 1438 TTGTCCACATTGCCGTTGAATGGCCCCCGTTGCAAAGGTTGGAGGTTTTTGGGGATGTTG 3632 1438 TTGCACATTGCCGTTGAATGGCCCCCGTTGCAAAGGTTGGAGGTTTTTTCTCCGA 3692 1448 AGTACAGTTGCTTGAATTCAAAGATCTAGAAACTTTTTTTT	1558 GGGGTGGTTCTGAAATAAAGTTGGGCGTGGACTAGTCGAAGGCCTTTGTGTTTACTTCC	1858 GAGCGCATCATATTGGCAAAGCAATGAGATATTGTGATAAAGCAACAACTGTCTCTAATA 1917 4053 GAGCCATCATATTGGTAAAGCAATGACATCTGATAAAGCACACACA	2098 AGAAGTTTGGGTTACAGCAAATCGATGCCCGTAGGAATCGTCACTCGCCTGACAG 2157 4293 AGAAGTTTGGATTACAGCAAACTGATGCCGTATTGTCGGAATCGTCACCCGTCTGACAG 4352 2158 CCCAAAAGGGGATCCACTCAACATGCGTATTGTCGGAATCATCACCCGTCTGACAGC 2217 4353 CCCAAAAGGGAATCCACTCATCAAGCACGCAATTCACCGAAAGCACTCGAAGGAACCAGAC 4412 2218 AGGTGGTTTTGCTTGATCAGCACGCGAATTCACCGAACTCTCGAAAGCAACGACC 4472 4413 ATGTGGTTTTGCTTGGTTCAAGCACGCAATCACAGACTGATTTTGCAAAGCACACGAC 2337 4413 ATGTGGTTTTGCTTGGTTCAACCAGGCAATCACGAACAGACGATTTTGCAAAGCACACGACC 2337 4473 CCGATGCTTTTGCTTGGTTCACTGGTAGGGTGAATCCTTGACCTACAAAGCAGAGC 2337 4473 CCGATGCTCTCATGGTTTACCATGGTAGGTGAAGCTTTCTTGACCTATGATGAGC 2337 4473 CCGATGCTCTCATGATAACGCTGGACTTCATATTTTGAGACTATATTTGAGC 4532 2338 CTCTCTCGCATCATAAACCTGGACTTCATAATTTTGAGACTATATTTGAGAC 4592 CTCTTCTCACCTGATAAAACGCTGGACTTCATAATTCTGGAAC 4592 CTCTTTCTCACCTGATAATACGCTGGACTTCATAATTCTGTACATTCAAACTTCGAAC 4592 CTCTTTCTCACCTGATAATACGCTGGACTTCATAATTCTGAACCTATAATTTGAAC 4592 CTCTTTCTCACCTGATAATACGCTGGACTTCATAATTCTTGAACTTCCAAACTTCGAAC 4592
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TGAAGAAAAGAAAAGGAAACTTGAGAGAGTTGCCACTGAAGAAGGAGGAGGGGGGGG	SIBS GAACACAIGITGATAATTIGTGGCCATAGAGCCTAGCAATATAGACAAGGGGACACTG 3247 601 TCAGATTGTATTATAACATAAACTCAAGACCTCTAGTTCACAGTACTGAGATATGGATGC 660 3248 TCAGATTGTACTATAACAGAAACTCAAGGCCGCTTATGCATAGTACTGGATGC 3307 661 ATGGTGGCTATAACAATTGATGATGGACTCTCTTTTGCTGAAAGGCTTGTTCATC 720 1308 ATGGTGGTTGCAATAGTTGGACTGATGGACTCTTTTGTAAAGACTTGTCATCATC 7337	ATGACAAAGATTGTGATTGGTGGTTTGCAGATGTTGTCGTGCCTGAAAGAACATATGTAT	### ##################################	961 AAAGGAAGGCTGAGAAAATGCAAAAATGAAAGCTGAGATGAAGGAAAAGACTATGAGAA 1020 3608 AAATAAAGGTTGAGAAAAAAAAAATGAAAATCTGAGATGAGAAAAGACTTATGAGAA 3667 1021 TGTTCCTGGTTTCTTGAAAACACTTGTTTACACCGAACCTTGAAATACTGGAAA 1080 1021 TGTTCCTGGTTTCTTAAAAACACTTGTTTACACGGAACCTTGAAATACTGGAAA 1080 3668 TGTTCTACTTTCTCAGAAACACATTGTTTATACTGGAACCACTTGAAATACGTGCTGGAA 3727			321 GGTTAGACTATCATATTCCTGTTTTTTGGGTCAATTGCAAGGAACCACCTATGCACATTG 968 GGACAGACTATCATATTCCTGTTTCTGGTTCCAATGCAAGGAGCTCCCATTGTATTGTTTCTGGTTCCAATGCAAAGGACTCCCCATTGTATTGTGTTCAATGCAATGCAAAGGTTGAAGGTCTTGGTGATGTTGTTGTTGTTGTTTGT

2581 TGAACAGGGCGAT 2593 |||||||| 5186 TGAACAGGCAAAT 5198

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Hayashida, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Pujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramcto, K., Hiracka, T., Hori, P., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kadagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa Hirozahe, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodawa, T., Kojima, K., Matsuwamata, T., Misura, J., Miyazaki, A., Masuda, H., Matsubara, C., Kurosaki, T., Kushimoto, N., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Mikura, J., Miyazaki, A., Maramura, M., Namiki, T., Narkawa, R., Niikura, J., Miyazaki, A., Nakamura, M., Namiki, T., Narkawa, R., Niikura, J., Nishi, K., Oka, M., Ooka, H., Osato, N., Otemo, Y., Ryu, R., Satoh, K., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, D., Sato, K., Satoh, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sagabe, Y., Sugami-Takeda, Y., Tagami, M., Tagami, M., Yamada, H., Yamamoto, M., Vasunishi, A., Yazaki, J., Vokomizo, S., and Yoshimura, A., Takahashi, F., Takaku-Akahira, S., Yokomizo, S., and Yoshimura, M., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., Silio, M., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Collection, mapping, and annotation of 28K full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kikuchi, S., Satoh, K., Magata, T., Kawagashira, N. Doi, K., Kikuchi, S., Satoh, K., Magata, T., Kawagashira, N. Doi, K., Kishimoto, N., Yazaki, J. Ishikawa, M., Yamada, H., Ooka, H., Hetta, I., Kojima, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizun, Y., Yoshimura, A., Miura, J., Kwani, Y., Carninci, P., Adachi, J., Alzawa, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Alzawa, K., Ishibiki, Y., Ichh, M., Hayalas, M., Watsubara, K., Ishidi, Y., Ichh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Vochi, N., Manda, R., Shiraki, T., Vochi, N., Manda, M., Shinagawa, A., Shiraki, T., Vochi, N., Manda, M., Shinaki, T., Vochi, N., Manda, M., Shinak
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AKLZZU98 11near PIN 29-OCT-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J033125F11, full
insert sequence.
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                                                                                                                                                                                                                                  AK122008.1 GI:37991744
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head claboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
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Science 301 (5631), 376-379 (2003)
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Unpublished
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TICE: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagate,T., Kawagashira,N., Doi,K., Kikhimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
PalS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Robayashi,M., Kodama,T., Kuroshaki,T., Kusumegi,T., Lu,M.,
Kobayashi,M., Midan,Y., Mizuno,K., Narikawa,R., Nikura,J., Oka,M.,
Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M.,
Xia,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
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Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Ittoh,M., Kagawa,J., Carninot,P., Kondo,S., Konno,H., Konda,M.,
Kishi,Rawa-Hirozane,T., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,H., Sakai,T.,
Sakai,C., Satoh,H., Sakai,T., Sagah,K., Tagami,M.,
Tagami-Takeda,Y., Tagawa,T., Tomaru,A., Toya,T., Waki,K.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunlshi,A. and Hayashizaki,Y.
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                         This clone is one of the 32K full-length cDNA clones from japonica
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/mol type="mRNA"
/cultivar="Wipponbare"
/db xref="taxon:39947"
/clone="J033125F11"
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rel:81-29-838-7007, Fax:81-29-838-7007)
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Sequence 131 from Patent WO03000905.
AX755430
AX755430.1 GI:32167798

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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1043 AIGACGAAAATGGTGATTGGTGGTATGC------TAATGCCTGAAAAGGCCTTTGTAT 1094
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Patent: WO 03003095-A 131 03-JAN-2003;
Syngenta Participations AG (CH)
Location/Qualifiers
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Pred. No. 0;
0; Mismatches

    .3032 /organism="Oryza sativa" /mol_type="unassigned DNA" /db_xref="taxon:4530"

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ilarity 77.5%;
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Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzeae, Oryza.
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Query Match 57.8%; Score 1500.4; DB 6; Length 4121; Best Local Similarity 74.4%; Pred. No. 0; Matches 1934; Conservative 0; Mismatches 601; Indels 63; Gaps 1;	1 AGCTTGCTGAAAAATTATTCGCTGGGAAACAAGTTGTTTACTTATCCAGATGTATTGA 60	61 AAGCTGATTCAACAATTGATCTGTTTTCAATCGTGATCTACCAGCTGTGGCCAATGAGC 120	121 CTGATGTACTTATGAAAGGAGCATTCAATGGGTGGAAGTGGAGATTTTTCACTGAAAAAT 180 	181 TGCACAAGAGCGAGCTGGGACTGGTGCTGCAAACTATACATTCCTAAGCAGG 240 	241 CATACAGAATGGACTTTGTGTTTTTTAACGGACACGCGTATATGAAAATAATAAATA	301 ATGATITCGTGATACAAATAGAAAGCACCATGGATGAAATTTATTT	361 CTGAAGAAAAGCAACGAGAACTTGAGAACCTTGCAAATGAGGAAGCTGAAAGGAAGG	421 AAACTGATGAGCGGGGGGAATGGGGAAGAAGAAGGGCCGCGGATAAAGCTGACAGGTAC 480 	481 AAGCCAAGGITGAGGTAGAGAAGAATAAATTGTGCAATGTATTGGGTTTAGCCA 540 	541 GAGCTCCTGTIGATAATTTAIGGTACATTGAGCCCATCACGACTGGACAAGAGGCTACTG 600 	601 TCAGATTGTATTATAACATAAACTCAAGACCTCTAGTTCACAGTACTGAGATATGGATGC 660 	661 ATGGTGGCTATAACAATTGGATTGATGTCTCTTTTGCTGAAAGGCTTGTTCATCATC 720 	721 ATGACAAAGATTGTGATTGGTGGTTTGCCAGATGTTGTCGTGCCTGAAAGAACATATGTAT 780 	781 IGGACHGGGTITTTGCTGACGGCCCACCAGGGGAGTGCAAGGAATTATGACAATGAGAG 840 	841 GACATGATTTTCATGCTACCCTTCCAAATAACATGACTGAGGAAGAGTATTGGATGGA	901 AAGAACAAAGGATCTATACAAGGCTTCAACAAGAGGAGAGAGA	961 AAAGGAAGGCTGAGAGAAATGCAAAAATGAAAGCTGAGATGAAGGAAAAGACTATGAGAA 1020 	1021 TGTTCCTGGTTTCTCAGAAACACATTGTTTACACCGAACCACTTGAAATACATGCTGGAA 1080
OME	& Q	Ž ₽	გ დ	≿ છ	≥ 9	£ 4	≿ 8	≿ ક	À 9	દ્ર ક	상 원	8 8	gp &	5 G	දු පු	S 8	강 염	8

ي ۾	318 CGTTTCTGCTCTCACAAAAACATATTGTGTATACTGAGCCAC	A 23
A A	1081 CTATATTGATGTGCTTTATAATCCTTCTAATACASTTCTAAC. 2378 CCACTGTGGACGTTCTTTATAATCCTTCTAACAGTGCTGAA.	
ži g	1141 GGITICGAIGTICCITTAAICGITGGAIGTAAICCAGGIGGGGIG 	GTTGCCACCTCAGAAGA 1200
ر الم	1201 IGGTACAAGCAGAAAATGGTTCACACCTAAAAGCAACAGTTTACC 	CGTTCCACGAGATGCCT 1260
λζ. Q0	1261 ATATGATGGACTTCGTTTTCTCGGAGTCAGAAGAAGGAGTTGAATTTAT 	TTATGATAACAGAAATG 1320
ZZ Q	1321 GGTTAGACTATCATATTCCTGTTTTTGGGTCAATTGCAAAGGAAC 	ACCACCTATGCACATTG 1380 AcctCCAATGCATATTG 2677
ે જ	1381 TCCACATTGCTGTTGAGATGGCACCAATGGCAAGGTTGGAGGT	CTTGGTGATGTTGTCA 144
<i>≵</i>	1441 CTAGTCTTTCAOGTGCTGTGCAAGATTTAGGACACAATGTGG 	TEGAGGTTATTCTTCCAAAGT 1500
<i>₹</i> ; q	1501 ACGGTTGCTTGAATCTAAGCAATGTCAAGAATCTACAAATCC 2798 ATGATTGTTTAATCCTAAGCAGTGTGAAGGATTTACACTACC	CATCAGAGITITICITGGG 1560
<i>≿</i> ; ;	561 GTGGTTCTGAAATAAATGTGTGGCGTGGACTAGTCGAAGGC	TTACTTCCTGG 162
9 25	AGAGGIAAAGITI AAAATGGGATGTTTGGAGTC	TGACCGCCGAT 168
qC	rraggirga	dargagragar 297
λ; q;	1681 TIGGCITCITCIGICGITCIGCICIAGAGITICICCICCAAAGIGG	TEGATCTTCTCCGAACA 1740
. qo	1741 TAATACAFTGCCATGATTGGTCAAGTGCTCCTGTTGCCTGGCT)	
74 ee	1801 CGAAGTCTAGCTAGGCAACGCACGGGTGGTATTCACCATCC 	CCATCCACAATCTTGAATTTTGGAG 1860
2y 0b	861 CGCATCATATTGG 1 158 CGCATCACATTGG	CAACTGTCTCTAATACAT 1920
Š S	921 ATTCAAAGGAAGTGTCAGGTCATGGTGCTACGTTCC	TCATCITGGGAAATTCTATGGCA 1980
ò	981 TTCTCAATGGAATTGATCCGGATATATGGGAT	CCGGTCC 204
q	ogaaariddarddreadarridddar	serrc 333
S A	2041 ACTACACTTGAGAATGTGGTTGAAGGCAAGAGGCTTG	
λ	2101 AGTTTGGGTTACAGCAAATCGATGTCCCCGTCGTAGGAATCGTC	CACTCGCCTGACAGCCC 2160

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LEGKGAAKKALQQMLGLQQTDSPVVGITRLTVQKGTHLLIKHAMHRALERNGQVVLLG
SAPDHRIQGDPTNLASKLHGEVHGRVKLCLTVDEPLSHLLIAMRYGSIPIVRYTGGLY
DATPDVDDRDRAQQQGLEDNGFSFEGADSSGVDYALDRAITAFYDARDMFNSLSKRV
MEQDNSWNRPALDYRALYGSRKN"
                          ODFHAIVPNNISDDIFWVEEEHRIFTRLQQERRERESAERIKAERSAKMKAEMKEKTM
RAFILSQKHIVYTEPLEVRAGTTVDVLYNFSNTVLNGKSEVWFRGSFNRWTHPSGPLP
                                                                                                                     PPMHIVHIAVEMAPIAKVGGLGDVVTSLSRAVQDLGHKVEVILPKYDCLILSSVKDLH
YQQSFASGGTEVKVWFGKVEDLPVYFILBPQNGMFWVGCVYGKNDBSRFGFFCHGALLEF
                                                                                                                                                                                LLOKGSSPDIIHCHDWSSAPVAWLYKEQYALNGLGNGRIVFTIHNLEFGAHHIGKAMA
                                                                                        POKAVKAENSSHLRTTVSVPLDAYAMDFVFSESEGGRYDNRNGMDYHI PVSDSVARB
YNNWIDGLSIAERLVKSHEKEGDWWYVEVTLPERALVLDWVFADGPPGNARNYDNNGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATACAGAATGGACTTTGTGTTTTTTAACGGACACACGGTATATGAAAATAATAACAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGATITITICCIGGAAATAGAAGAGACATAGATGAACACTCATITGAGGACTICTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1658 Trigaagaaaaggaaaggaacricgaggcrirgcrgcagaagacrigaaaggaaaagac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1718 AAGCTGAGGAGCGCCACAGGAGGAAGAAAGGGCCGCGGATGGAAGCTGACAGGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1838 GCAGATATGCTGAGAACTTATGGTACATAGAACCTAACACCTACAGAGGAGGAGACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 CTGAAGAAAGCAACGAGAACTTGAGAACCTTGCAAATGAGGAAGCTGAAAGGAGGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      4121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1500.4;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 74.4%; Pre
Matches 1934; Conservative 0;
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NGSLYGEAAEQASTAEESSQVYMTGDILSGAERDGAGTEEEBADQNQSSALPSASMDDD
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//prodein_id="CAB40374.1"
//protein_id="GL40874.1"
//db_xref="GL408760"
//db_xref="GD4098GG0"
//db_xref="GD408GG0"
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DNSIPVPYTAENVVEGKRASKEALQQKLGLKKADLPLVGVI TRLTHQKGIHLIKHAIN
RTLERGGQVVLLGSAPDHRIQNDFVNIANQLHSSHNDRARLGLAYDPPLSHMIYAGAD
FILVPSIFEPCGLTQLTAMRYGSIPIVRKTGGLYDTVFDVDNDKDRAQVQGLEPNGFS
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DCLALSNVKDLQFHKSFWGGTBTKVWHGKVEGLSVYFLEPQNGLFWYGCYGRANDA
BRRGFFCHAALBFLLQNGSHPDIIHCHDWSSAPVAWLFKEQYTHYGLSKARVVFTIHN
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                                                                                                                                                                                               db_xref="taxon:3917"
id. .360#
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BC mmber="2.4.1.21"
/function="ADP-glucose-starch glucosyltransferase"
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                                                                          organism="Vigna unguiculata"
|mol type="mRNA"
|cultivar="C-88"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1217.6;
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VGTKLYBILQVDVEPQQLKENNAGHVEYKGEVASKLIBITKASDVBHTESNEIDD
NEPFKEDILEDDEPLAAGTVETGDSSLNLIRLEMEANLERQAIERLAEBNLLQGIR
PEPVVKPDEDVEIFURGLSTLKNESDVLINGAFNEWRYRSFTTRLTETHLNGDN
KKHYPKEAYRADEVPFNGQDYYDNDGNDFSITVKGGMQIIDENFLLEEKWREQ
AKRQAERBELAEEQRRIEABEKAEIEADRAQAKKERAAKKKVLRELMYKATKTRDI
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YYTEVVIPDQALFLDWVFADGPPKKALAYDNHKQDFHAIVPHHIPEELYWVEEE
FKTLQEBERLREAAMRAKVEKTALLKTETKERTMKSFLLSQKHVVYTEPLDIQAG
IVYYNPANTVLNGKPEI WEFFERENTEGEL PPPGHASPAENGTHVRAYDLAMPKYPYESEREDGGTPDNKSGMDYHIPVFGGYBPMHIVHIAYDLAYBMAPIAKVKGL
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DOVYTSELSRAVQDLMHVNDILLLEKTOLKMNNYKOFFFHKWNFWGGTFEIKWFGGYEG
LSVYTSELSRAVQDLMHVDILLLEKTOLKMNYKOFFFHKWNFWGGTFEIKWFGKVBG
LSVYTSELSRAVQDLMHVDGERFGFFCHAALEFLLOGGFSPDIHGKDWSSAP
VAMLFREQYTHYGLSKSRIVFTHNLEFGADLIGRAMTVADKATTVSFTYSGEVSGNP
VLAPHHKFGTVNGIPDDIMDPLNYFFIFIFSTRVVVCFGTYAAKTGALGKA
DLPLVGIITTRLTHQKGIHLIKAALFRTLERNGGVVLLGSAPDFRVQNNFVNLANQLHS
KXNDRARLCLTYDBELSHLIYAAADFILVPSFIFFENGGVYLLGSAPDFRVQNNFVNLANGLHS
YDTVFDVVDHNKERAQQCGLERNGFSFTGFARAKTGGL
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/db_xref="SWISS-PROT:Q43846"
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SWRDGMVTGVSFSICANFSGRRRRRVSTPRSQGSSPKGFVPRKPSGMSTQRKVQKSN
GDKESKSTSTSKESELSNOKVTVSARVETSDDTKGVVRDHKFLEDEDELNGSTKSISM
SPVRVSSQFVBSEETGGDDKDAVKLNKSKRSEESGFIIDSVIREQSGSGQGETNASSKG
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LDTNSFFKSDLIEEDEPLAAGTVETGDSSLNLRLEMEANLRRQATERLAEENLLQGIR
LFCFPEVVKPDEDVETFLNRGLSTLKNESDVLIMGAFNEWRYRSFTTRLTETHLNGDW
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UK
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                                                                                                                                                                        TGGAGGGCTCTTCGACACTGTCTTCGATGTGGACAATGACAAGGAACGAGCCCGAGATCG
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                                                                                                                 TTGCGGCCTAACTCAGCTCGTCGCCATGCGGTATGGAACCATCCCGATTGTCCGCAAGAC
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product="glycogen (starch)
protein_id="CAA65065.1"
db_xref="GI:1200154"
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/cultivar="Desiree"
/db.xref="taxon:4113"
/tissue type="tuber"
/clone lib="lambda gt11"
/43. .3835
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Plant Cell 8 (7), 1121-1135 (1996)
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Submitted (19-FEB-1996) A.
Norwich, Norfolk NR4 7UH, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGAACAGGGCGATCTCAG 2598
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Solanum tuberosum
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Edwards, A.
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SSYTVYYNPAATVYLNGKPEINFRCSFRRWTHLGPLPPCKMSPAENGTHYRAYKVPDL
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Organism="Solanum tuberosum"
|mol_type="mRNA"
|cultivar="Desiree"
|db_xref="taxon:4113"
| ..4167
                                                                                                                                                                                                                                                                                                                                                                                         protein id="CAA64173.1"

db_xref="G1:1911166"

db_xref="GOA:Q43846"

db_xref="SWISS-PROT:Q43846"
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CATAATACATTGCCATGATTGGTCAAGTGCTCCTGTTGCCTGGCTACGAGGAAAACTA
CGCGAAGICTAGCTIGGCAAACGCACGGGTGGTAITCACCAICCACAAICTIGAAITIGG
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AIATICAAAGGAAGIGICAGGICAIGGGCGIAGAGITCCICAICITGGGAAAITCIAIGG
CATTCTCAATGGAATTGATCCGGATATATGGGATCCGTACAATGACAACTTTATCCCGGT
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TGGAGGGCTCTTCGACACTGTCTTCGATGTGGACAATGACAAGGAACGAGCCCGAGATCG
AGGCCTTGAGCCCAACGGGTTTAGCTTTGACGGAGCTGATAGCAACGGTGTTGACTACGC

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(IOWA) UNIV IOWA STATE RES FOUND INC. 97US-00968542 WPI; 1999-327406/27. James MG; P-PSDB; AAY06199 Myers AM,

Nucleic acid encoding starch synthase enzyme of maize.

Claim 1; Page 104-107; 138pp; English

This is the nucleotide sequence of the maize gene dull1 (du1). To tagging strates was used to isolate the gene and describe its a transposon tagging stratesy was used to isolate the gene and describe its properties product. The invention reports tagging of the du1 locus with whitensposon, cloning and characterisation of a portion of the gene, and isolation a near full-length cDNA (the present sequence). The amino acid sequence (see AAYO6199) deduced from this cDNA indicates that Du1 codes of SIII. Its expression pattern indicates that Du1 codes for SIII. Its expression pattern indicates that Du1 codes for SIII its expression pattern indicates that Du1 codes for SIII its expression pattern indicates that Du1 codes for SIII of maize endosperm. The Du1 product contains unique sequence features in its N-biosynthetic enzymes. Mutations within the maize SIII gene affect multiple aspects of starch biogenesis by disrupting an enzyme complex containing starch synthace(s), starch branching enzyme(s) and possibly starch debranching enzyme(s). The isolated cDNA can be used to provide an enzyme with which to regulate the production of starch, and with which to regulate the production of starch, and with which to produce altered or novel forms of starch, e.g. in transgenic plants. Expression of Du1 in bacteria and yeasts also modifies glycogen production. Claimed expression vectors comprise the cDNA or fragments of it that code for functional portions of DU1.

Sequence 6027 BP; 1800 A; 1177 C; 1441 G; 1609 T; 0 U; 0 Other;

; Length 6027; DB 2; 0 100.0%; Score 2598; 100.0%; Pred. No. 0; tive 0; Mismatches Best Local Similarity 100. Matches 2598; Conservative Query Match ਨੋ

CATACAGAATGGACTTTGTTTTTTTAACGGACACACAGTATATGAAAATAATAACAATA 2724 2425 AGCTTGCTGAAAAATTATTCGCTGGGAAACAAGTTGTTTACTTATCCAGATGTATTGA 2484 2485 AAGCTGATTCAACAATTGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCAATGAGC 2544 2605 IGCACAAGAGCGAGCIGGCAGGGGACIGGIGCIGCAAACIAIACAIICCIAAGCAGG 2664 2545 CTGATGTACTTATCAAAGGAGCATTCAATGGGTGGAAGTGGAGATTTTTTCACTGAAAAT 2604 CTGAAGAAAAGCAACGAGAACTTGAGAACCTTGCAAATGAGGAAGCTGAAAGGAGGAGAC 2844 AAGCTGATTCAACAATTGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCAATGAGC 120 CTGATGTACTTATCAAAGGAGCATTCAATGGGTGGAAGTGGAGATTTTTCACTGAAAAT 180 CATACAGAATGGACTTTGTGTTTTTTAACGGACACACGGTATATGAAAATAATAACAATA 300 CTGAAGAAAAGCAACAAGAACTTGAGAACCTTGCAAATGAGGAAGCTGAAAGGAGGAGAC 420 9 1 AGCTTGCTGAAAAAATTATTCGCTGGGAAACAAGTTGTTTACTTATCCAGATGTATTGA TGCACAAGAGCGAGCTGGCAGGGGACTGGTGCTGCAAACTATACATTCCTAAGCAGG Gaps 181 241 301 2725 61 2665 2785 121 361 g ò 엄 ð q à d g ò DP à ò

λõ	N	TGATGAGCAGCGGCGAATGGAGGAAGAAGGGCCGCAGATAAAGCTGACAGGGTAC 48
qq	2845	AAACTGATGAGGAGGGGGGAATGGAGGAAGAAGGGCCGCGGAGATAAAGCTGACAGGTAC 2904
ογ	481	AAGCCAAGGTIGAGGIAGAGGAGGAAGAAGAATGAATGTGCAATGTATTGGGTTTTAGCCA 540
qu		AAGCCAAGGTTGAGGTAGAGAAGAAGAATAAATTGTGCCAATGTATTGGGTTTAGCCA 2964
ζ		AGAGGCTACTG 60
QQ	2965	GAGCTCCTGTTGATAATTTATGGTACATTGAGCCCATCACGACTGGACAAGAGGCTACTG 3024
, 02	109	TCAGATTGTATTATAACATAAACTCAAGACCTCTAGTTCACAGTACTGAGATATGGATGC 660
Db	3025	TCAGATTGTATTATAACATAAACTCAAGACCTCTAGTTCACAGTACTGAGATATGGATGC 3084
ζζ	661	AUGGIGGCIADAACAAITGGAITGAIGGACICICITITIGCIGAAAGGCIIGITCAICAIC 720
qq	3085	AIGGIGGCIATAACAATIGGAITGAIGGACICTTITGCIGAAAGGCTIGTICATCAIC 3144
à	721	AIGACAAAGAIIGIGAIIIGGGGGIIIGGGAGAIGIIGGIGGGGCCTGAAAGAACAIAIGIAI 780
DP	3145	AIGACAAAGAIIGIGATIGGIGGIIIGCAGAIGTIGICGIGCCIGAAGAACAIAIGIAI 3204
λŏ	781	TGGACTGGGTTTTTGCTGACGCCCACCAGGGAGTGCAAGGAATTATGACAACAGGAG 840
Db		IGGACTGGGTTTTTGCTGACGGCCCACCAGGGAGTGCAAGGAATTATGACAACAATGGAG 3264
ζŏ	841	GACATGATTTTCATGCTACCCTTCCAAATAACATGACTGAGGAAGAGAATTGGATGGA
QQ	3265	GACATGATTTTCATGCTACCCTTCCAAATAACATGACTGAGGAAGAGTATTGGATGAAG 3324
δy	901	AAGAACAAAGGATCTATACAAGGCTTCAACAAGAGGAGGGAAGGGAGGAGGAGGGCTATTA 960
qa		AAGAACAAAGGATCTATACAAGGCTTCAACAAGAGGAGGAGGAAAGGAGGAGGAGGAGTTTTA 3384
ογ		AAAGGAAAGGCTGAGAGAAATGGAAAATGAAAGCTGAGAAAGAA
Db	3385	AAAGGAAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAGGAAAGAATATGAAAA 3444
δλ		IGITCCIGGITICTCRGAAACACATIGITIACACCGAACCACTIGAAAIACAIGCIGGAA 1080
Db	3445	TGTTCCTGGTTTCTCAGAAACACATTGTTTACACCGAACCACTTGAAATACATGCTGGAA 3504
ζŏ	1081	•
Db	3505	ACTATTGATGTGCTTTTATAATCCTTCTAATACAGTTCTAACTGGAAAGCCAGAGGTTT 356
δλ	1141	TTCGATGTTCCTTTAATCGTTGGATGTATCCAGGTGGGGGTGTTGCCACTCAGAAGA 120
Db	3565	GGTTTCGALGTTCCTTTAATCGTTGGATGTATCCAGGTGGGGTGTTGCCACCTCAGAAGA 3624
Qy	1201	TGGTACAAGCAGAAAATGGTTCACACCTAAAAGCAACAGTTTACGTTCCACGAGATGCCT 1260
ηp	3625	TGGTACAAGCAGAAATGGTTCACACCTAAAAGCAACAGTTTACGTTCCACGAGATGCCT 3684
δy	1261	ATATGATGGACTTCGTTTTCTCGGAGTCAGAAGAAGGTGGAATTTATGATAACAGAAATG 1320
ΩÞ	3685	ATATGATGGACTTCGTTTTCTCGGAGTCAGAAGAAGGTGGAATTTATGATAACAGAAATG 3744
<i>\$</i> 3	1321	GGTTAGACTATCATATTCCTGTTTTTGGGTCAATTGCAAAGGAACCACCTATGCAATG 1380
qq	3745	GGTTAGACTATCATATTCCTGTTTTTTGGGTCAATTGCAAAGGAACCACCTATGCACATTG 3804
δy	1381	TCCACATIGCTGTIGAGAIGGCACCAATCGCAAAGGTIGGAGGTCTIGGIGAIGTIGTCA 1440
Db	3805	TCCACATTGCTGTTGAGATGGCACCAATCGCAAAGGTTGGAGGTCTTGGTGATGTTGTCA 3864
Qy	1441	CTAGTCTTTCACGTGCTGTGCAAGATTTAGGACACAATGTGGAGGTTATTCTTCCAAAGT 1500
QQ	3865	JICTTTCACGTGCTGTGCAAGATTTAGGACACAATGTGGAGGTTATTCTTC

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2485 AAGCTGATTCAACAATTGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCCAATGAGC
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5005 TGAACAGGGCGATCTCAG 5022
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                                                                              ABX09935 standard; DNA; 6027
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                3925 ACGGTTGCTTGAATCTAAGCAATGTCAAGAATCTACAAATCCATCAGAGTTTTTCTTGGG
                                                                                                          AACCTCAAAATGGGATGTTTGGAGTCGGATATGTATATGGCAGGGACGATGACCGCCGAT
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  1501 ACGGTTGCTTGAATCTAAGCAATGTCAAGAATCTACAAATCCATCAGAGTTTTTTCTTGGG
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The invention describes an isolated DNA molecule encoding a fusion protein consisting of 4 different functional domains selected from glucan association domain (GLASS), linker dunctional domains selected from glucan association domain (GLASS), linker dunctional consisting of the cerminal end (CTEND) which are operably linked to domain (GLYRR), and C-terminal end (CTEND) which are operably linked to one another. The DNA molecule is useful for expressing in plants of moluding starch and modified catalytic capabilities and to improved affinity to starch and modified catalytic organilities and to the in vivo and in vitro synthesis of glucan chains of modified lengths as compared to plants producing native starch produced with cative starch synthases. Expression of the starch synthase fusion proteins along with granule bound starch synthase (GBSS) will lead to a modified starch having an altered or improved morphology, retrogradation, waterbinding, or swelling potential of the granules, gel strength, adhesiveness, cohesiveness, hardness, elasticity, increased or decreased con decreased glucan chain lengths. This sequence concodes a starch synthase used in the invention
                                                                                                     domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA encoding fusion protein consisting of 4 different functional domains selected from glucan association domain, linker domain, glucosyl transferase domain, and C-terminal end, useful for producing modified
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                                                                                            Starch; starch synthase; glucan association domain; GLASS; linker in the Allorsey luransferase domain; GLYTR; C-terminal end; CTENN; granule bound starch synthase; GBSS; mcrphology; retrogradation; waterbinding; swelling potential; gene; ds.
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DNA encoding maize Starch synthase III (Du1).
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Query Match Best Local Similarity

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composition, and to screen plants to identify mutations which affect starch content and composition. The starch can then be used in food products, such as flour, and in films, coatings, adhesives, building 88888

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Db	1775 GGA	
λŏ	1375 ACATTO	TIGICCACATIGCTGTIGAGAIGGCACCAATCGCAAAGGTIGGAGGICTIGGTGGIG 1434
Db	1835 GTA	IG 18
δy	1435 TTG	GICACTAGICTITICACGIGCIGIGCAAGAITIAGGACACAAAGGGGGGGTAATICTIC 1494
qu	1895 TTG	CC 19
ογ	1495 CAAA(TT 15
Ор	1955 CGA	-E
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qq	2015 CTT	CT 20
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à	75	TC 173.
qo	35	- TC 219
λŏ	1735 CGAAC	AA 17
qq	2195 CAC	AC 22
λò	1795 ACT	ACGCGAAGTCTAGCTTGGCAAACGCACGGGTGGTATTCACCATCCACAATCTTGAAT 1854
qq	2255 ACT	ATTCCCAATCCAGAATGGCAAGGACTCGGGTTGTATTTACCATCCACAATCTTGAAT 2314
à	1855 TTG	Fi
qq	2315 TTG	gaagarcattatattggtaaaggaatgacatactgtgataaagggacacaactgtttctc 2374
δ.	15	CT 197
Dp	2375 CTÀ	CATATICAAGGGACGTGGCAGGCCATGGCGCCATTGCTCCTCATCGTGAGAATTCT 2434
8 8	975 ATG	SCATTCTCAATGGAATTGATCCGGATATATGGGATCCGTACAATGACAACTTTATCC 203
ga	9	SCATTCTCAATGGAATTGATCCAGATATCTGGGGATCCGTACACTGACAATTT

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The present invention relates to a method (MI) for identifying genes involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an unifected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

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pathogenic infection for conferring resistance or tolerance to a bacterial, fungal or viral infection by determining or detecting gene expression.

SEQ ID NO 3150; 899pp; English

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Indels

497;

Score 1703.8; Pred. No. 0; 0; Mismatches

65.6%;

Query Match Best Local Similarity 79.2 Matches 2054; Conservative

Н 2648 61

0;

DB 7; Length 5760;

Sequence 5760 BP; 1762 A; 988 C; 1429 G; 1576 T; 0 U; 5 Other;

AGCTTGCTGAAAAATTATTCGCTGGGAAACAAGTTGTTTACTTATCCAGATGTATTGA AACTTGCTGACCAGAATTGTTCAATGGGTAACAAGCTTTTCGTTTTTTCCAGAGGCAGTGA AAGCIGAITCAACAATIGAICTCIATITCAAICGIGAICTAICAGCIGIGGCCAAIGAGC 120

2708 AGGCTAATTCGACAATTGATGTATTTTGAATCGTAACCTATCGGCTTTGGCGAATGAGC

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CIGAIGICCACAICAAAGGAGCAIICAAIAGIIGGAGAIIGGAGGCCIIICACCGAAAGAC
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Whitham S, Xie Z,
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(first entry)

20-NOV-2003

Rice gene, SEQ ID 3150

Plant; gene;

3007

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3187

3247

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щ× Cooper 3, Tao

Chen W, C

Chang H, Katagiri

WPI; 2003-175290/17.

(SYGN) SYNGENTA PARTICIPATIONS

22-JUN-2001; 2001WO-IB001105 22-JUN-2001; 2001WO-IB001105

WO2003000898-A1 Oryza sativa

03-JAN-2003

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3368 ATGACGAAAATGGTGATTGGTGGTATGCTAATGTTCATATACCTGAAAAGGCCTTTGTAT 3427 781 TGGACTGGGTTTTTGCTGACGGCCACCAGGGAGTGCAAGGAATTATGACAACAATGGGG 840 3428 TGGACTGGGTTTTTGCTGACGGCCACCTGGAAATGCAAGGAATTATGACAACAATGGTC 3487 841 GACATGATTTTCATGCTACCCTTCCAAATAACAGAAGGAAATTATGGATGG	61 61 21 68	114 378 120 384	1201 TGGTACAAGCAGAAATGGTTCACACCTAAAGCAACAGTTTACGTTCCACGAGATGCCT 1260	1321 GGTTAGACTATCATATTCCTGTTTTTGGGTCAATTGCAAAGGAACCACCTATGCACTTG 1380	1441 CTAGTCTTTCACGTGCTGTGCAAGATTTAGGACACAATGTGGAGGTTATTCTTCCAAAGT 1500 4088 CAAGTCTTTCACGTGCAATTCAAGAGTTAGGCCATCATGTTGAGGTTATTCTCCCGAAAT 4147 1501 ACGGTTGCTTGAATCTAAGCAATGTCAAGAATCTACAAATCCATCAAAGTTTTCTTGGG 1560 4148 ATAATTTTATGAATCAAAAGCAATGTGAAGAATTTGCATGTACAAAGCTTTTCTTGG 4207	1561 GTGGTTCTGAAATAAATGTGGGGTGGACTAGTCGAAGGCCTTTGTGTTTACTTCCTGG 1620	1681 TTGGCTTCTTCTGTCGTTCTGAGAGTTTCTCCTCCAAAGTGGATCTTCTCCGAACA 1740

δ	1861 CGCATCATATTGGCAATGAGATATTGTGATAAAGCAACAACTGTCTCTAATACA	T 1920
q	4508 CACATTTATTGGAAAAGCAATGACATACTGCGACAAAGCCACAACTGTTTCTCACACG	r 4567
λŏ	1921 ATTCAAAGGAAGTGTCAGGTGCCATAGTTCCTCATCTTGGAAAATTCTATGGCA	198
쉼	4568 ATTCAAAGAAAGTCGCAAGGTCATGGTGCCATAACTCCTCATCGTGGAAAATTCTATGG	4627
δ	1981 TECECARIGAATEAECGGAFATATATGGGATCCGTACAATGACACTTTATCCGGGTCC	204
qq	4628 TTCTCAATGGAATTGATCCAGATATCTGGGATCCATATACTGATAACTTCATCCGGAT	468
ð i	04	A 2100
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QQ	α0 α0	0 C
8 8	2161 AAAAGGGATCCACCTGATCAAGCATGGGATTCACCGTACACTCCAACGGAACGGAACAGG 200 AGAACGTATCACCTTATTAAACATGCACTTCATGGGACTTTAAGGGAATGGACAGGAAGACACTTGAAGGGAATGAACACTTGATGAACTATTATATATA	G 2220 G 4867
3 - 6		22
ž 43	898	492
ò	2281 ATACGCTCCACGCGTAAACCATGGGCAAGTGAGGCTTTCCTTGACCTACGACGAGCC	C 2340
q	4928 ATAGICITCATGGTGAAAACCATGG	- 4952
δ	2341 TCTCGCATCTGATATACGCTGCTCTGACTTCCATTCTGGTCCCATCTATTTGAGCCTT	T 2400
qq	4953CAGGATATATGCTGGCTCTGACTTCATCCTTGTTCCATCCA	T 5005
Š	2401 GCGGCCTAACTCAGCTCGTCGCCATGCGGTATGGAACCATCCCGATTGTCCCGAAGACTG	'G 2460
Db	5006 GCGGTTTGACTCAACTTGTTGCCATGCGCTATGGATCCATCC	.d 5065
οy	2461 GAGGGCTCTTCGACACTGTCTTCGATGTGGACAAGGAACGAGCCCGAGATCGAG	AG 2520
qq	5066 GAGGACTTTACGACACTGTTTTCGACGTAGACCATGACAAAGACCGGGCTTCGAGTTCT	kĠ 5125
δŏ	2521 GCCTTGAGCCCAACGGGTTTAACTTTTGACGGAGCTGATAGCAACGGTGTTGACTACTACGCGC	7
g	5126 GCCTTGAACCAAATGGGTTCAGCTTTGATGGAGCTGACTGTAATGGTGTGGATTACG	3¢ 5185
Š	2581 IGAACAGGGGGT 2593	
qq	5186 TGAACAGCAAAT 5198	
RESUI ADA7(JIT 6 10734 BDB 70734 standard: DNA: 3645 BP.	
X		
\S	ADA70734;	
ž Ei	20-NOV-2003 (first entry)	
岩 智	Rice gene, SEQ ID 4057.	
a io	Plant, bacterial infection, fungal infection, viral infection, rice gene, ds.	15
X S	Oryza sativa.	
Z E S	WO2003000898-A1.	
\$B\$	03-JAN-2003.	

gene

(SYGN) SYNGENTA PARTICIPATIONS 22-JUN-2001; 2001WO-IB001105 22-JUN-2001; 2001WO-IB001105 Cooper S, Tao s, WPI; 2003-175290/17 Quan × Chen Chang H, Ch Katagiri F,

response of a plant of ing plant Identifying at least one gene involved in plant resistance or respathogenic infection for conferring resistance or tolerance to a bacterial, fungal or viral infection by determining or detecting expression.

t t

Claim 6; SEQ ID NO 4057; 899pp; English

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fundal or viral infection. The present sequence was used to invention illustrate the

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Sequence 3645 BP; 1101 A; 688 C; 905 G; 949 T; 0 U; 2 Other;

ö 120 AGCITGCTGAAAAATTATTCGCTGGGAAACAAGTTGTTTACTTATCCAGATGTATTGA Gaps Length 3645; , 0 Indels 7; 593; DB ; Score 1646.8; I ; Pred. No. 0; 1; Mismatches 5 63.48; Conservative Query Match Best Local Similarity Matches 2002; Conserv Н 926 ð g $\overset{>}{\circ}$

crdaratrorrarcaaagggggarrcaarggriggagarggaaaaarrracccaaaaa 1105 recaraaaacreacriaacaeeeearreereerecrecaaacrecararecaaeeee TGCACAAGAGCGAGCTGGCAGGGACTGGTGCTGCAGAACTATACATTCCTAAGCAGG 1106 1046 181

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1440 1500 21.25 1320 1620 2065 1705 rcaaarrgrrcracaacagaagcrcaagaccgcraargcaraacacrgagarrrggargc 1585 ragacrosorritrocroargescraccrossariscaaggaritargaracaariscac 1765 840 AAAGGAAGGCTGAGAAAATGCAAAAATGAAAGCTGAGATGAAGGGAAAAGACTATGAGAA TGTTCCTGGTTTCTCAGAAACACATTGTTTACACCGAACCACTTGAAATACATGCTGGAA 1946 ACTITCITCICCICGCAGAAACACATIGIGIACACIGAGCCICTCGAAGIACGIGCAGGAA CTACTATTGATGTGCTTTATAATCCTTCTAATACAGTTCTAACTGGAAAGCCAGAGGTTT reciesas recesas de recentrados en recentrados en recentrados en recentrados recentrados en recen ATATGATGGACTTCGTTTTCTCGGAGTCAGAAGAAGTGGAATTTATGATAACAGAAATG ATATGATGGACTTTGTTTTTCTCTGAGTCGGAAGAAGATGGAATATATGACAACAGGAATG GGTTAGACTATCATATTCCTGTTTTTGGGTCAATTGCAAAGGAACCACCTATGCACATTG GCATGGACTATCATAGTCCTGTGACTGATTCCGTTGCAAAAGAACTCCTATGCATATTG TCCACATTGCTGTTGAGATGGCACCAATCGCAAAGGTTGGAGGTCTTGGTGATGTTGTCA recacarrecagradaaarescrecrarrecaasstressescrerresrearistra CTAGTCTTTCACGTGCTGTGCAAGATTTAGGACACAATGTGGAGGTTATTCTTCCAAAGT caagretricacdagecerreagarirageceacaarerreaggriarrerreceagr ACGGTTGCTTGAATCTAAGCAATGTCAAGAATCTACAAATCCATCAGAGTTTTTCTTGGG ATGACTGTTTAAACCTAAGCAATGTGAAAGATTTACATTACCGTCAAAGTTTTACTTGGG GTGGTTCTGAAATAAATGTGTGGCGTGGACTAGTCGAAGGCCTTTGTGTTTACTTCCTGG draaracadagaraadrarddrrriddaaaddrrgaadaccccidrrracridc 1621 AACCICAAAAIGGGAIGIIIIGGAGICGGAIAIGIAIAIGGCAGGGACGAIGACCGCCGAI AACCACAGAATGGGATGTTTTGGGTTGGATGTGTCTATGGAAGAAATGACGAGAGTAGAT ATGGTGGCTATAACAATTGGATTGATGGACTCTTTTTGCTGAAAGGCTTGTTCATCATC 1766 gecaggarriccargerierrerrecaaaraacararcreaggacergrirregergaag AAGAACAAAGGATCTATACAAGGCTTCAACAAGAGGAGGGAAAGGGAGGAGGCTATTA GAAGAAAGTCTGAGATAACTGCAAAAATGAAAGCTGAGATGAAGGAAAAAGACTATGAGAG ccacceredarerreracaarecereraacaceerecreaacedaaacecadaeerrr GGTTTCGATGTTCCTTTAATCGTTGGATGTATCCAGGTGGGGGTGTTGCCACCTCAGAAGA gerreagarerrecritraareerregaereareeagreereerregeegeagaaa TGGTACAAGCAGAAAATGGTTCACACCTAAAAGCAACAGTTTACGTTCCACGAGATGCCT TGGACTGGGTTTTTGCTGACGGCCCACCAGGAGTGCAAGGAATTATGACAATGGAG GCAGATATGCTGATAATCTATGGTATATAGAGCCTCACCATACAAAGCAGGGGATAGGG Argecegitacaaraatiecagicafiegecreteratiecreaaaarraarcaaatear ATGACAAAGATTGTGATTGGTGGTTTGCAGATGTTGTCGTGCCTGAAAGAACATATGTAT 2186 2246 2306 1441 2366 1501 2426 1561 2486 1081 2006 1141 2066 1201 2126 1261 1321 1381 781 1706 1021 1526 1586 1646 901 1466 661 841 601 721

Rice DNA sequence Seq ID131 related to grain filling.

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ADC07865 RESULT

(first entry)

18-DEC-2003

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This invention, in the area of plant biotechnology, relates to novel polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, what, and rice. The invention may be useful for the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a more data for this patent did not form part of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formed directly from WIPO at
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                                                                        plant biotechnology, carbohydrate synthesis, carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; corn; tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain; gene; ds; plant.
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Pred. No. 0;
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Kreps J, P
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26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
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Best Local Similarity 77.5%;
Matches 2048; Conservative
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Glazebrook J, Katagiri F
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P-PSDB; ADC07866.
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This invention describes a novel nucleic acid (1) encoding a protein (11), or its active fragments, with starch synthase (SS) activity encoding a 1170 residue amino acid sequence (SS), comprising a 1121 base encoding a 1170 residue amino acid sequence (SS), comprising a 121 base pair sequence (SI), both fully defined in the specification, or its complement, or containing the coding region of the cDNA insert in plasmid (R65/87 (DSM 12970) or its complement. The invention also describes (1) vector containing (1) (1), (2) host cell, or transgenic plant cell, that contains (I) or the vector of (1), or is derived from such a cell; (3) (II), or its active fragments, encoded by (I); (4) production of (II), or its active fragments, encoded by (I); (5) plant containing cransgenic cells of (2), and their replicative material; (6) production of the plants of (5); (7) starch produced by the plant cells of (2) or the plants of (5), or their replicative material; and (8) production of modified starch by extraction from the plant cells of (2) or the plants
                                                                                                            2535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding a starch synthase isoform from maize, used to
produce recombinant plants that produce starch with modified properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthesis; starch synthase; maize; transgenic plant; nutrition;
2666 IGCIGGCICTGACTICTIGIICCAICCAITCAACTIGGAGTIIGACICAACI
                                                                                                                                            CIGITITICGACGIAGACCAIGACAAAGACCGGGCICGAGITCIAGGCCITGAACCAAAIG
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                                     CGTCGCCATGCGGTATGGAACCATCCCGATTGTCCGCAAGACTGGAGGG-CTCTTCGACA
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product= "starch synthesis associated protein"
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442. 3954
/*tag= a
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of (5), or their starch-storing parts. (I) is used to prepare transgenic plants (specifically maize) that have reduced or increased SS activity, resulting in formation of starch with different chemical and/or physical, and functional, properties, particularly altered viscosity and gelforming properties. Fragments of (I) can also be used as probes to isolate related sequences from other organisms, also as attisense inhibitors of SS activity. The starch produced by the transgenic plants is useful for all usual nutritional and non-nutritional applications. Modified starch may be better suited to particular applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGACTGGGTTTTTGCTGACGGCCCACCAGGGAGTGCAAGGAATTATGACAACAATGGAG
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                                                                                                                                                                                           Sequence 4121 BP; 1180 A; 829 C; 1119 G; 993 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                          0; Mismatches 601; Indels
                                                                                                                                                                                                                                     DB 5;
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Pred. No. 0;
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Best Local Similarity 74.4%;
Matches 1934; Conservative
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901 AAGAACANAGGATTTCCTAATAACATATACGATGATATATCGGATGATATTCGGTGGAAG 2197 901 AAGAACANAGGATTTCATACAAGGCTTCAACAAGAGAGAGAGAGAGAG	GTGGTTCTGAAATAAATGTGGGCGTGACTAGTCGAAGCCTTTGTGTTTACTTCTGGGTGCCAAAAGGTTGAAAGGTTGAAGGTTTACTTCTTGGTGCACAGGCACAGGACTGTTTACTTCTTGGTGCACAGGACAGAGAGCCTTTACTTCTTGGTAAAAGGTTGAAAGGTTGAAAGGTTGAAAGGTTGAAAAGGTTGAAAGGTTGAAAGGTTGAAAGGTTGAAAGGTTGAAATGCAAAATGGAAGAATGAAAAAGAAAAAAAA

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                                                                                                                                                                                                                                                                                                                                                           A composite cDNA sequence (AAMT68646) codes for a a 100-140 kDa potato soluble starch synthase (AAW17785). The sequence was deduced from 2 overlapping cDNA clones obtd. from a tuber cDNA library by immunoscreening with antiserum raised against purified starch synthase. Starch synthase nucleic acids can be linked to a plant promoter, in sense or antisense direction, and used to alter starch characteristics in transgenic plants, esp. potato, tomato, rice, wheat, peal cassava, sweet potato, barley, oar or maize. A novel altered starch, extracted from such transgenic plants, has a viscosity onset temperature that is reduced by at least 5 degc compared to starch from non-transformed plants. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                           Soluble starch synthase - used to produce altered starch from commercially important plants, e.g. potato, rice, wheat, and maize.
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Fred. No. 0;
0; Mismatches
                                                                                                                                                                                  Martin
                                                                                                                                                                                  EA,
                                                                                                                                                                                                                                                                                                                                  16; Page 18-24; 39pp; English
                                                                                                                                                                                    Edwards
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Best Local Similarity 66.7%;
Matches 1735; Conservative
                                                                        96EP-00309004
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                                                                                                                                                                                    Smith AM, Marshall J,
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(SYGN) SYNGENTA PARTICIPATIONS

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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
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                                                                             Nucleic acid molecules encoding wheat starch synthase (WST)-1 and WST-II, useful in modifying plant starch content and/or composition.
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                                                                                                                                                                                                                                     The present invention relates to novel protein and coding sequences f wheat. The proteins are wheat starch synthases, designated SSII and SSIII. These can be used in the modification of plant starch content composition, and to screen plants to identify mutations which affect starch content and composition. The starch can then be used in food products, such as flour, and in films, coatings, adhesives, building materials and packaging materials
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                                                                                                                                                                                      Claim 1; Page 187-188; 211pp; English
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/transl_except= (pos:310. .312, aa:Xaa)
/transl_except= (pos:406. .408, aa:Xaa)
/note= "Xaa corresponds to unknown amino acid; CDS does
not include start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthase; DU1; enzyme; transgenic plant; genetic mapping;
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synthase DU1 homologue cDNA #2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel protein and coding sequences from wheat. The proteins are wheat starch synthases, designated SSII and SSIII. These can be used in the modification of plant starch content or composition, and to screen plants to identify mutations which affect starch content and composition. The starch can then be used in food products, such as flour, and in films, coatings, adhesives, building materials and packaging materials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and WST-II,
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Pred. No. 5.8e-137;
0; Mismatches 185; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 200-206; 211pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appels R;
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(LIMA-) GRP LIMAGRAIN PACIFIC PTY
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Local Similarity 76.8%;
ses 612; Conservative C
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                                                                                                                                                                                                                                 Wheat SSIII gene SEQ ID NO:
                                 781 TGGACTGGGTTTTTGCT
                                                                                                                                                                                                                                                               Wheat; starch synthase;
food product; adhesive;
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P-PSDB; AAE20906.
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(BECK/) BECKLES D M
(THOR/) THORPE C J.
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                                                                                                                      Oryza sativa
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                          01-JUL-2002
                                                     Rice starch
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                                                                                                                                                                                                 The invention relates to isolated starch synthase DU1 homologue polypeptides and their polymucleotides. The polymucleotide is useful for polypeptides and their polymucleotides. The polymucleotide and transforming transforming a cell and for producing a transforming a plant cell with the polymucleotide and regenerating a plant from a plant cell with the polypeptide is useful for preparing antibodies. The polymucleotide is useful for preparing antibodies. The polymucleotide is useful for creating in mapping the gene that they are a part of, and as markers for traits. In they are a part of, and as markers for traits transgenic plants in which the polympclede is present at higher or lower transgenic plants in which the polympclede is present at higher or lower levels than normal or in cell types or developmental stages in which they can be not normally found, for altering the level of starch synthesis and carbohydrate composition in the plants, and to design and produce primers or probes. The present sequence is rice starch synthase DU1 homologue con a probes.
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                                                                                                                         Novel isolated starch synthase DUI homolog polypeptide and polymucleotide which is useful for transforming a cell and producing a transgenic plant having altered level of starch synthesis and carbohydrate composition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1781 GCTACACAAAGGAAAACTACGCGAAGTCTAGCCAAAACGCACGGGTGGTATTCACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 548 BP; 156 A; 121 C; 113 G; 155 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 79.9%; Pred. No. 2.9e-75;
Matches 341; Conservative 0; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD33324 standard; cDNA; 437 BP.
                                                                Thorpe CJ;
                                                                                                                                                                                     Claim 8; Page 15; 18pp; English
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                                                                 Beckles DM,
                                                                                            WPI; 2002-291589/33.
             ALLEN S M.
BECKLES D M.
THORPE C J.
                                                                                                           P-PSDB; AAE20907
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             (ALLE/) F
(BECK/) F
(THOR/) 1
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The invention relates to isolated starch synthase DU1 homologue compositions and their polymucleotides. The polymucleotide is useful for polympeptides and their polymucleotides. The polymucleotide is useful transforming transforming a plant cell with the polympelotide and regenerating a plant from a composition of the polympeptide is useful for preparing antibodies. The polympeptide is useful for preparing antibodies. The polympeptide is useful as probes for genetically and physically companing the gene that they are a part of, and as markers for traits contained to those genes. The polymucleotide is useful for creating contained to those genes. The polymucleotide is useful for creating contains in which the polympeptide is present at higher or lower contained the polympeptide is useful stages in which they can be composition in the plants, and to design and produce primers or probes. The present sequence is rice starch synthase DU1 homologue contains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated starch synthase DU1 homolog polypeptide and polynucleotide which is useful for transforming a cell and producing a transgenic plant having altered level of starch synthesis and carbohydrate composition.
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                                                                                                                                                                                                                                                                                                                        product= "Rice starch synthase DU1 homologue protein"
'Anote= "CDS does not include start and stop codon"
                                                    starch synthase; DU1; enzyme; transgenic plant; genetic mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 207.6; DB 6;
Pred. No. 1.2e-50;
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synthase DU1 homologue cDNA #1.
                                                                                                                                                                                                                                    location/Qualifiers
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Best Local Similarity 72.3%;
Matches 295; Conservative
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2431 ATGGAACCATCCCGAATTGTCCGCAAGACTGGAGGCTCTTCGACACTGTCTTCGATGTGG 2490
                                                    2550 GGAGCTGATAGCAAC-GGTGTTGACTACGCGCTGAACAGGGCGATCTC 2596
                                                                                       362 GGAGCTGACANCAACGGGTGTGGATTACCCCCTTGACAAGCNATCAC 409
2 d 2 d
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Search completed: June 20, 2004, 05:39:54 Job time : 1462 secs

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Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 9, Appli Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli 
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2598
1 agcttgctgaaaaaaattat......gctgaacagggcgatctcag 2598
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Sequence
Sequence
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1: /cgp12_6/ptodate/2/ina/5A_COMB.seq:*

1: /cgp2_6/ptodate/2/ina/5B_COMB.seq:*

3: /cgp2_6/ptodate/2/ina/6A_COMB.seq:*

4: /cgp2_6/ptodate/2/ina/6B_COMB.seq:*

5: /cgp2_6/ptodate/2/ina/PCTUS_COMB.seq:*

6: /cgp2_6/ptodate/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-111-704-1

US-09-111-704-1

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US-09-345-214-16
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US-09-345-214-15
US-09-345-214-15
US-09-345-214-20
US-09-743-980-15
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Maximum Match 100%
Listing first 45 summaries
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Sequence 1, Application US/09554467A

Patent No. 6639125

GENERAL INFORMATION:

APPLICANT: Myers, Alan M.

APPLICANT: James, Martha G.

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

CURRENT APPLICATION NUMBER: US/09/554,467A

CURRENT FILING DATE: 1990-11-12

PRIOR APPLICATION NUMBER: US 08/062,102

PRIOR FILING DATE: 1997-11-12

WHOBE OF SEQ ID NOS: 37

LENGTH: 6027
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                                 Indels
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    Best Local Similarity 66.7%; Pred. No. 0;
Matches 1735; Conservative 0; Mismatches 862;
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kossmann, Jens
APPLICANT: Springer, Franziska
APPLICANT: Springer, Franziska
APPLICANT: Abel, Gernoc
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
NUMBER OF SEQUENCES: 17
    2520
                                                                                                                             3755 GCCTCGAGCCAAATGGATTCAGTTTCGAAGGAGCTGATAGCAGTGGTGTAGATTATGGTC 3814
                                      3695 GAGGCCTGTACGACACCGTCTTTGACGTCGACGATGATAAGGATCGGGCTCAAGCACAAG 3754
2461 GAGGGCTCTTCGACACTGTCTTCGATGTGGACAATGACAAGGAACGAGCCCGAGATCGAG
                                                                                         GCCTTGAGCCCAACGGGTTTAGCTTTGACGGAGCTGATAGCAACGGTGTTGACTACGCGC
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CURRENT APPLICATION DATA:
PLILCATION WIMBER: US/08/836,567
FILING DATE: 24-CUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
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PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P44 41 408.0
FILING DATE: 10-NOV-1994
ATTOREY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: Agrevo-4
TELEPRENCE/DOCKET NUMBER: Agrevo-4
TELEPRENCE/DOCKET NUMBER: Agrevo-4
TELEPRENCE, 212-596-9000
TELEPRAX: 212-596-9000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LUMOTH: 4168 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08836567 Patent No. 6130367
                                                                                                                                                                                  2581 TGAACAGGCGATCTCAG 2598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN: cv. Dsire
TISSUE TYPE: leaf tissue
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STRANDEDNESS: single
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307..3897
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LIBRARY: CDNA-
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; LOCATION:
US-08-836-567-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: N
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                46.4%; Score 1204.8; DB 4; Length 4168; llarity 66.7%; Pred. No. 0; Conservative 0; Mismatches 862; Indels 3;
                                                                                                                                                                                                                                                                             LIBRARY: cDNA-library in Lambda ZAPII OTHER INFORMATION: CDS
                                                                                                                                                                                                                                                                                                                                            LOCATION: 307..3897
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-606-304-11
                                                                                                                                                                                             ORGANISM: Solanum tuberosum
                                                                                                                                                                                                                 STRAIN: cv. D, sir, e
TISSUE TYPE: leaf tissue
IMMEDIATE SOURCE:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4168 base pairs
                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA tO RNA
ORIGINAL SOURCE:
                                                                                  TYPE: nucleotide
STRANDEDNESS: single
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Best Local Similarity
Matches 1735; Conserva'
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qo	96 GAGAATAGATGGTGATTGGTGGTATACAGAGGTTGTTATTCCTGATCAGGC	
g ç	782 GGACTGGSTITTTGCTGACGGCCCACCAGGGAGTGCAAGGAATTATGACAAC	AATGGAGG 841 ATCACCG 2015
2y. 0b	842 ACATGATTTTGATGCTACCCTTCCAAATAACATGACTGAGGAGGAGTATTGGAT 2016 CCAAGACTTCCATGCCCTTGTCCCCAACCACATTCCGGAGGAATTATATTGGGT	NTGGAAGA 901 YTTGAGGA 2075
75. 25.	902 AGAACAAAGGATCTATACAAGGCTTCAACAAGAGGAGGGAAAGGGAGGG	GCTATTAA 961 GCTATGCG 2135
ζ,	SCTGAGAGAAATGCAAAATGAAAGCTGAGATGAA	TGAGAAT 102
qq		TGAAATC 2195
% 9	1022 GTICCIGGITICTCAGAACACATIGITIACACCGAACCACTIGAAAIACATI 	GCTGGAAC 1081 GCTGGAAG 2255
Oy Db	1082 TACTATTGATGTGCTTTATAATCCTTCTAATACAGTTCTAACTGGAAAGCCA 2256 CAGCGTCACAGTTTACTATAANCCCGCCAATAAAGGTAATAAAGTAAAAGAAAAAGAAAAAAAA	CCAGAGGTTTG 1141
ζ	142 GTTTCGATGTTCCTTTAATCGTTGGATGTATCCAGGTGGGGGTGTTGCCAG	120
qq	316 Gricagardircarrraardgerggacreacegecreggreeardgeded	-5
음 당 음	1202 GGTACAAGCAGAAATGGTTCACACCTAAAAGCAACAGTTTACGTTCCACGAG.	AGATGCCTA 1261 GGATGCATA 2435
à	TTTTTCTCGGGGTCAGAAGAAGGTGGAATTTATGATAAC	GAAATGG 132
qq	GATGGATTTTGTATTTTCCGAGAGAGAAGATGGTGGGATTTTTGAC	
λ	322 GITAGACTATCATATTCCTGTTTTTGGTCAATTGCAAGGAACCACCTA	FTGT 138
Q O	496 AATGGACTATCACATACCTGTGTTTGGAGGAGTCGCTAAAGAACTCCAAT	ratig
Sy Db	1382 CCACATTGCTGTTGAGATGGCACCAATCGCAAAGGTTGGAGGTCTTGGTGAT	GTTGTCAC 1441 GTTGTTAC 2615
ά	NTTTAGGACACAATGTGGAGGTTATTCTT	AAGTA 150
qq	CITICCCGIGCTGTTCAAGATTTAAACCATAATGTGGATATTATCTTA	 CCTAAGTA 2675
λά	502 CGGTTGCTTGAATCTAAGCAATGTCAAGAATCTACAAATCCATCAGAGTTTT	TCTTGGGG 1561
qq	76 IGACIGITIGAAGAIGAATAAIGIGAAGGACITICGGITICACAAAACIAC	irirgege 2735
Sy Dp	1562 IGGTTCTGAAATAAATGTGTGGCGTGGACTAGTCGAAGGCCTTTGTGTTTACT	TCCTGGA 1621 TTTTGGA 2795
λa	1622 ACCTCAAAAIGGGAIGTTTGGAGTCGGATATGTATATGGCAGGGACGATG	ACCGCCG 1678
QC QC	2796 GCCTCAAAACGGGTTATTTTCGAAAGGGTGCGTCTATGGTTGTAGCAATGATG	 GTGAACG 2855
ζλ	CGTTCTGCTCTAG	CTCCGAA 1738
qq	deritcircidicacececiriceaciticirciecaae	GTCCGGA 2915
ž	739 CATAATACATTGCCATGATTGGTCAAGTGCTCCTGTTGCCTGGTACA	AAAAC
qu	16 TATCATTCATTGCCATGATTGGTCTAGTGCTCCTGTTG	AACAATA 2975
δλ	1799 GGCGAAGTCTAGCTAGCACAGCAGGGTGGTATTCACCATCCACAATCTTGAATTTGG	AATTTGG 1858 [

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763 CTGAAAGAACATATGTATTGGACTGGGTTTTTTGCTGACGGCCCACCAGGGAGTGCAAGGA
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35.8%; Score 931; DB 3; Length 2303;
Best Local Similarity 68.5%; Pred. No. 2.2e-284;
Matches 1301; Conservative 0; Mismatches 595; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: 3..2033
; COTHER INFORMATION: /function= "Polymerization of starch";
CTHER INFORMATION: /product= "Starch synthase"
US-08-836-567-1
                                                                                              OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-ULL-1997
CLASSIFICATION NUMBER: DS/08/415
FILING DATE: 26-ULL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 44 41 408.0
FILING DATE: 09-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: Agrevo-4
TELEPHONE: 212-596-9000
TELEPHONE: 212-596-9000
TELEPHONE: 212-596-9000
SUNDEMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
THANKALL STARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: cDNA-library in pBluescriptSKII+
                        COMPUTER READABLE FORM in TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Solanum tuberosum
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STRANDEDNESS: unknown
TOPOLOGY: linear
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
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TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
NUMBER OF SEQUENCES: 17
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                                             AGCGCATCATATTGGCAAAGCAATGAGATATTGTGATAAAGCAACAACTGTCTCTAATAC
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                                                                                         3036 GGCAGATCTCATTGGGAGGGAATGACTAACGCAGACAAAGCTACAACAGTTTCACCAAC
                                                                                                                                       ATATTCAAAGGAAGTGTCAGGTCATGGTGCCATAGTTCCTCATCTTGGGAAATTCTATGG
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ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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Patent No. 6130367
GENERAL INFORMATION:
APPLICANT: Kossmann, Jens
APPLICANT: Springer, Franziska
APPLICANT: Abel, Gernot
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US-08-836-567-1
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OTHER INFORMATION:
OTHER INFORMATION:
/product="Starch synthase"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as.08%; Score 931; DB 4; Length 23 Similarity 68.5%; Pred. No. 2.2e-284; D1; Conservative 0; Mismatches 595; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: cDNA-library in pBluescriptSKII+OTHER INFORMATION: CDS
                                                                                                                                                                                                                                             ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum
STRAIN: CV Berolina
TISSUE TYPE: tuber tissue
                                 LENGTH: 2303 base pairs
TYPE: mucleotide
STRANDEDNESS: unknown
TOPOLGY: linear
MOLECTLE TYPE: DNA
HYPOTHETICAL: NO
SEQUENCE CHARACTERISTICS:
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Matches 1301;
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δλ	83 AGGTTATTCTTCCAAAGTACGGTTGC	TACAAATCC 15
Q O	TATTATCTTACCTAAGTATGACTGT	GAAGGACTTTCGGTTT
ζ	4	GIGGCGIGGACIAGICGAAGGCC 16
Dp	53 ACAAAACTACTTTTGGGGTGGG	91
ν	03 TITGIGITITACTICCIGGAACCI	9
qu	crcesicrarrirriesascci	attitcgaaagggigcgiciaiggit 972
ð i	60 GCAGGACGATGACCGCCGATTTGGCTTCTT	CTCC 171
Q	TAGCAATGATGGTGAACGATTTGGTTTCTT	GGCTTTGGAGTTTCTTCTGC 103
يع يې	1720 AAAGTGGATCTTCTCGAACATAATACATTGC	CATGATTGGTCAAGTGCTCTGTTGCCT 1779
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à t	1000 COCCIACACCACACACACACCACCACACACACACACACAC	CINGCILGGCAAACGCACGGGIGGIAIICACCA 103.9
ò	40 TCCACAATCTTGAATTTGGAGCGCATC	GTGATAAAG 189
qu	53 TACATAATCTTGAATTTGGGGCAGATCTCATT	\overline{a}
λ̈́o	JAACTGTCTCTAATACATATTCAAAGGA	STCAGGTCATGGTGCCATAGTTCCT
Db	1213 CTACAACAGTTTCACCAACTTACTCACAGGAGGT	
δχ	CTTGGGAA	CGGATATAT
Dp	1273 ACCTTCACAAGTTCCATGGTATAGTGATGGGA	CTTT
à	2020 AIGACATITAICCCGGICCACTACACTIGG	GAGAATGTGGTTGAAGGCAAGAGGGCTG 2079
qu	CGATAAGTTCATTCCGATACGTACCTCA	CAAAACAGCA
λŏ	TAAGAGGCACTGCAGCAGAAGTTTGGG	TTACAGCAAATCGATGTCCCCGTCGTAGGAA 2139
ηq	 	ACCTICCTITGGIA
δy	2140 TCGTCACTCGCCTGACAGCCCAAAAGGGGATCC	CCACCTGATCAAGCATGCGATTCACCGTA 2199
qq	TATCACCCGCTTAACTCACCAGAAAGGAAT	
δλ	2200 CACTCGAACGGAACGGACAGCTGGTTTTGCTTGGTTCAG	Б-
Db	1513 CCTTGGAACGGACAGGTAGTCTTGCTTC	TCCTGATCCTAGGGT
ò	2260 CTGATTTTGTCAACCTGGCGAATACGCTCCACC	CAAGTG
Db		GCACTCCAAATATAATGACCGCGCACGACTCT 1632
ογ	CTACGACGAGCCTCTCTCGCATCT	F-1
DÞ		TTTTATTCTA
70	2380 ICCCAICTATATTGAGCCTTGCGGCCTAACTC	GCTCGTCGCCATGCGGTATGGAACCA 2439
Db		
٥x	CCGATTGTCCGCAAGACTGGAGGGCT	CTTCGACACTGTCTTCGATGTGGACAATGACA 2499
Db	TCCAGTCGTGCGTAAACTGGAGGACT	TTGACCATGACA

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5.6%;
ilarity 51.4%;
Conservative
          2.0
     SOFTWARE: Patentin Ver.
SEQ ID NO 1
LENGTH: 2652
                                                                                                     NAME/KEY: CDS
LOCATION: (9)..(2213)
                                                                                                                                                                                       Similarity
                                                     TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                      Query Match
Best Local Simi
Matches 657;
                                                                                                                                   US-09-115-704-1
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GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN ETIE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGRAM
SEQ ID NO 101
LENGTH: 212
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APPLICANT: Kossmann, Jens
APPLICANT: Kossmann, Jens
APPLICANT: Froheerg, Claus
TITLE OF INVENTION: WHICH PARTICIPATE IN THE STARCH SYNTHESIS
TITLE OF INVENTION: WHICH PARTICIPATE IN THE STARCH SYNTHESIS
TITLE OF INVENTION: WHICH PARTICIPATE IN THE STARCH SYNTHESIS
CURRENT APPLICATION NUMBER: US/09/115,704
CURRENT FILING DATE: 1998-07.15
BARLIER APPLICATION NUMBER: PCT/EP97/00158
BARLIER FILING DATE: 1997-01-15
BARLIER APPLICATION NUMBER: DE 196 01 365.8
BARLIER PILING DATE: 1996-01-16
NUMBER OF SEQ ID NOS: 2
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                                                           2560 GCAACGGTGTTGACTACGCGCTGAACAGGGCGATCTCAG 2598
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OTHER INFORMATION: Incyte ID No. 6476212 700548531H1
NAME/KEY: unsure
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US-09-313-294A-101
; Sequence 101, Application US/09313294A
; Patent No. 6476212
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US-09-115-704-1
Sequence 1, Application US/09115704
; Patent No. 6211436
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OTHER INFORMATION: a, t, c, g,
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Best Local Similarity 94.8%;
Matches 200; Conservative
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ORGANISM: Zea mays
FEATURE:
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                                                                  Indels 150;
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      Length 2652;
Score 145; DB 3; I
Pred. No. 5.2e-35;
0; Mismatches 470;
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00 00 00 00 00 00 00 0	NESULT 10 10-509-780-115-1 Sequence 1, Application US/09780115 Sequence 1, Application US/09780115 Sequence 1, Application US/09780115 GENERAL INFORMATION: REPLICANT: Forberg, Claus APPLICANT: Forberg, Claus TITLE OF INVARITON: WHICH PARTICIPATE IN THE STARCH SYNTHESIS TITLE OF INVARITON: WHORER: US/09/780,115 CURRENT APPLICATION NUMBER: US/09/780,115 PRIOR FILING DATE: 1996-07-15 PRIOR FILING DATE: 1996-07-15 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR FILING DATE: 1996-07-16 PRIOR PRIOR FILING DATE: 1996-07-16 P

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COUNTRY:
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APPLICANT: Singletary, George
APPLICANT: Singletary, George
APPLICANT: Singletary, George
APPLICANT: Singletary, George
TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
TITLE OF INVENTION: Use in the Production of New Starches
FILE REFERENCE: 1146
CURRENT APPLICATION NUMBER: US/09/388,743
CURRENT FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Fastere for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2084 GAGGGCACTGCAGCAGAAGTTTGGGTTACAGCAAATCGATGTCCCCGTCGTAGGAATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2271 TATAAGGAAĞCATCTTAAACİTTCCİTGTCAGAGGGTTCİCGAÇCACİGGİTĞCTTGTAİ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2384 ATCTATATTTGAGCCTTGCGGCCTAACTCAGCTCGCCATGCGGTATGGAACCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 144.8; DB 4
Pred. No. 7.3e-35;
                                                                                                                                        Sequence 9, Application US/09388743
Patent No. 6423886
2489 GGACAATGACAAGGAAC 2505
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Maranta arundinacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 56.5%;
Matches 313; Conservative
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                                    1982 GGACGATGAAACGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KBY: CDS
; LOCATION: (1315)...(2913)
US-09-388-743-9
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3434
                                                                                                                     US-09-388-743-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-DEC-1995
CLASSIFICATION 800
PRIOR APPLICATION 800
PRIOR APPLICATION BOTA:
APPLICATION NUMBER: 08/346,602
FILING DATE: 29-NOV-1994
CLASSIFICATION BOTA:
APPLICATION NUMBER: 08/263,921
FILING DATE: 21-UN-1994
CLASSIFICATION NUMBER: 08/263,921
FILING DATE: 21-UN-1994
CLASSIFICATION NUMBER: 08/263,921
FILING DATE: 21-UN-1994
CLASSIFICATION NUMBER: 08/263,921
FILING DATE: 21-UN-1994
CLASSIFICATION NUMBER: 08/263,921
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CLASSIFICATION NUMBER: 08/263,921
FILING DATE: 21-UN-1994
CLASSIFICATION NUMBER: 08/263,921
FILING DATE: 21-UN-1994
CLASSIFICATION NUMBER: 08/263,921
FILING DATE: 21-UN-1994
CLASSIFICATION NUMBER: 08/263,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.3%; Score 111.8; DB 1;
36.0%; Pred. No. 1.6e-24;
ative 93; Mismatches 262;
Sequence 3, Application US/08572951
Patent No. 5824700.
GENERAL INFORMATION:
APPLICANT: KEELING, PETER L.
APPLICANT: KNIGHT, MARY E.
APPLICANT: GUAN, HANPING
ITILE OF INVENTION: MODIFICATION OF STARCH
ITILE OF INVENTION: SYNTHESIS IN PLANTS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             ADDRESSEE: CUSHMAN DARBY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: Pillsbury Madison & Sutro LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 222957/1.02.15C
TELECOMOUNICATION THORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2380 base pairs
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Best Local Similarity 36.0%
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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Gaps

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APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEMONIAE FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 20004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 3687
LENGTH: 1248
                                                                                                                                                                                                                                                                                              1446 caactracacerrosacacerecacacececcaacecacecacecacececcecceccececece 1505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCTCTCTCGCATCTGATATACGCTGGCTCTGACTTCATTCTGGTCCCATCTATATTTGA 2395
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                                                                                                                                                                                                                                                                                                                                                                                                                                     2156 AGCCCAAAAGGGGATCCACCTGATCAAGCATGCGATTCACCGTACACTCGAACGGAACGG
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                                                                                                                                                                                                                                                   2039 CCACTACACTTGTGAGAATGTGGTTGAAGGCAAGAGGGCTGCTAAGAGGGCCACTGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                     1956 CCTCATCTTGGGAAATTCTATGGCATTCTCAATGGAATTGATCCGGATATATGGGATCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2456 GACTGGAGGGCTCTTCGACACTGTCTTCGATGTGGACAATGACAAGGA 2503
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                                                                                                                                                       Length 2097;
                                                                                                                                                          Score 85.6; DB 3; Length 2:
Pred. No. 3e-16;
0; Mismatches 204; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1626 GCAGCTCGTGATGCTGGGCACCGGGCGGGCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3687, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3687
                                                                                                                                                            3.3%;
                                                                                                                                                          Query Match 3.3
Best Local Similarity 52.6
Matches 246; Conservative
              ORGANISM: Zea mays
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261; Conserv
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US-09-489-039A-3687/c
                                                              NAME/KEY: CDS
LOCATION: 1...
ORIGINAL SOURCE
                                                                                                            US-08-941-445A-10
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                                        FEATURE:
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Matches
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                                                                                                                                                                                                                                                                                                                              1858 YINAAYCARYINTAYGCNATGGCNTAYGGNACNGTNCCNGTNGTNCAYGCNGTNGGNGGN 1917
                     166 GGGATCCACCTGATCAAGCATGCGATTCACCGTACACTCGAACGGAACGGACAGGTGGTT 2225
                                                                 1633 GGNGTNGAYATHATHGCNGAYGCNATHCAYTGGATHGCNGGNCARGAYGTNCARYTNGTN 1692
                                                                                                                                                          1693 ATGYTNGGNACNGG-------NMGNGCNGAYYTNGARGAYATGYTNMGNMGN 1737
                                                                                                                                                                                                                                                1738 TTYGARWSNGARCAYWSNGAYAARGTNMGNGCNTGGGTNGGNTTYWSNGTNCCNYTNGCN 1797
                                                                                                                                                                                                                                                                                                                                                                                          CTAACTCAGCTCGTCGCCATGCGGTATGGAACCATCCCGATTGTCCGCAAGACTGGAGGG
                                                                                                              2226 TIGCTIGGTTCAGCGCCGGACTCTCGAATCCAAGCTGATTTTGTCAACCTGGCGAATACG
                                                                                                                                                                                                        2286 CTCCACGGCGTAAACCATGGGCAAGTGAGGCTTTCCTTGACCTACGACGAGCCTCTCG
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EILLING DATE: 30-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STRET: 5370 Manhattan Circle CITY: Boulder STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Realing, Peter
APPLICANT: Guan, Hamping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 69-97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-941-445A-10
; Sequence 10, Application US/08941445A
Patent No. 6107060
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: 1
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Search completed: June 20, 2004, 12:54:58 Job time: 222 secs
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA;
TITLE OF INVENTION: PREDWONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004/001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 3662
LENGTH.
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522 CAAAACGATCTGCTGCTGCCGATGCGCTACGATCGCGACACGCTGGAGGAGAAGGCGGAG
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Pred. No. 1e-15;
0; Mismatches 254; Indels 15
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3862
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Best Local Similarity 49.2%;
Matches 261; Conservative
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US-09-489-039A-3862
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1048 GGTCTGCTTGAGCAGCGCCCCAGCTGGCGCTTGCTGGGCCCGCCGGCGATCCGGTGCTGCAG 1107
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                                                                                                                     2256 CAAGCTGATTTTGTCAACCTGGCGAATACGCTCCACGGCGTAAACCATGGGCAAGTGAGG
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

June 20, 2004, 05:15:45 ; Search time 1495 Seconds Run on:

(without alignments) 7960.983 Million cell updates/sec

Title: Perfect score:

US-10-634-262-1_COPY_2425_5022 2598

1 agcttgctgaaaaaaattat.....gctgaacagggcgatctcag 2598

IDENTITY_NUC Scoring table:

Sequence:

3017426 segs, 2290544650 residues Gapop 10.0 , Gapext 1.0 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published Applications NA:* Database :

| Cgn2 6/ptodata/2/pubpna/US07 PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 1, Appli	Sequence 1145, Ap	Sequence 1, Appli	Sequence 11, Appl	Sequence 1, Appli	Sequence 20351, A	Sequence 30909, A	Sequence 97896, A	Sequence 4321, Ap	Sequence 91, Appl	Sequence 3, Appli	Sequence 83485, A	Sequence 1, Appli	Sequence 84418, A
SUMMAKIES		ID	US-10-634-262-1	US-10-109-048-1145	US-10-424-799-1	US-10-284-668-11	US-10-284-668-1	US-10-425-114-20351	US-10-425-114-30909	US-10-424-599-97896	US-10-425-114-4321	US-10-341-961A-91	US-09-739-438-3	US-10-424-599-83485	US-09-739-438-1	US-10-424-599-84418
		DB	13	17	15	15	15	13	13	13	13	16	σ	13	σ	13
		Match Length DB	6027	6027	3693	4168	2303	1338	2581	2218	1181	585	548	641	437	464
	* Query	Match	100.0	100.0	46.4	46.4	35.8	35.6	31.8	27.9	18.5	12.2	11.2	10.9	8.0	7.2
	,	Score	2598	2598	1204.8	1204.8	931	924.8	826.4	724.4	480.4	315.8	290.6	283.8	207.6	186.2
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	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence 3	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
9-294-093B-334	94-093B-352	-10-424-599-1099	10-425-114-338	US-10-163-214-1	1-10-044-543-9	10-163-214-	-163-214-1	4	-163-214-	US-10-369-493-33677	1-10-424-599-29678	10-424-599-2	-10 - 36	1-10-425-114-14355	-10-369-493-3	-352	10-369-493-4	10-425-114-864	-10 - 13	-10-424-59	10-369-493-4	-10-369-493-3506	-10-369-493-3	-10-369-493-386	-10-369-493-389	-10-425-114-3	-10-425-114-105	10-336-753-4	-10-109-048-114	8-10-369-493-38452
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OTHER INFORMATION: cDNA sequence corresponding to the gene encoding the COTHER INFORMATION: starch synthase enzyme DU1. US-10-634-262-1 TYPE: DNA ORGANISM: maize US-10-634-262-1 FEATURE:

DB 13; Length 6027; Indels 100.0%; Score 2598; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Query Match Best Local Similarity Matches 2598; Conserv

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61 AAGCTGATTCAACAATTGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCAATGAGC 120

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Db 2665 CATACAGAATGGATTTTTTTAACGGACACGGGTATATGAAAATAATAACAATA 2724	661 ATGGTGGCTATAACATTGGATTGATGGATTGCTGTGCTG
QY 2281 ATACGCTCCACGGCCTAAACCATGGGCAAGTGAGGCTTTCCTTGACCTACGACGAGGCCTC 2340 4705 ATACGCTCCACGGCGTAAACCATGGGCAAGTGAGCTTTCCTTGACCTACGACGAGGCCTC 4764 QY 2341 TCTCGCATCTGATCTGACCTGACTTCCTTGACCTATATTTGAGCCTT 2400 A765 TCTCGCATCTGATCTGACTCTGACTTCATTCTGGTCCCATCTATATTTGAGCCTT 2401 A765 TCTCGCATCTGATCTGACTTGACTTCATTCTGGTCCCATCTATATTTGAGCCTT 2461 A826 GCGCCTAACTCAGTCGCTGACTTGACTTCATTCTGATCCCCATCTATATTTGAGCCTT 4824 A827 CTGGCCTAACTCAGCTGGTGCTTGACTTCATTCTATATTTGAGCCTT 4884 A828 GCGGCCTAACTCAGTCGCTGGCTATGACTACCATCCGATTGTCGCAAGACTG 4884 A828 GCGGCCTAACTCAGTCGCATGGGACAATGACAAGACCAGACCGCAAGACTGAGGCTGATGACTACAGACTGAGGCCCCAAGACTGACAAGACTGACT	RESULT 2 UG-10-109-049-1145 UG-10-109-049-1145 Publication No. US2004107451A1 Sequence 1145, Application US/10109048 Publication No. US2004107451A1 APPLICANT: REMIREZ, NOWER, PETER L. APPLICANT: RAMIREZ, NOWER AND SETER L. APPLICANT: MCKEAN, ANGELA MATCHG 2299; Conservative 100.0%; Score 2598; DB 17; Length 6027; Best Local Similarity 100.0%; Score 2598; DB 17; Length 6027; Matchg 2299; Conservative 0; Mismatches 0; Indels 0; Gaps 0; MATCHG 2299; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ANGERT MCKEANAANATHATTCGCTGGGAAACTATTCTATCCAGATGACTATCCAGAACTAGCTGGAAACTAGACTA

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QY 2461 GAGGGCTCTTCGACACTGTCTTCGATGACAATGACAAGGAACGAGCCCGAGATCGAG 2520 Db 4885 GAGGCTCTTCGACACTGTCTTCGATGTGACAATGACAACGAGCCCGAGATCGAG 4944 QY 2521 GCCTTGAGCCCAACGGGTTTAGCTTTGACGAGACGATAGCAACGGTGTTACTACTACGCGC 2580 Db 4945 GCCTTGAGCCCAACGGGTTTAGCTTTGACGAGCTGATAGCAACGGTGTTGACTACGCGC 5004 QY 2581 TGAACAGGGGATCTCAG 2598 Db 5005 TGAACAGGGCGATCTCAG 5022	SULT 3 -10-424-799- Suguence 1, Dublication GENERAL INFO APPLICANT: TITLE OF INTILE OF	Qy 482 AGCCAAGGTTGAGGTAGAGGACGAAGAATAAATTGTGCAATGTATTGGGTTTAGCCAG 541
1381 TCCACATTGCTGTTGAGATGGCACCAATCGCAAAGGTTGGAGGTCTTGGTGATGTTGTCA 1440 3805 TCCACATTGCTGTTGAGATGGCACCAATCGCAAAGGTTGGAGGTCTTGGTGATGTTGTCA 3864 1441 CTAGTCTTTGAGATGGCACCAATCGCAAAGGTTGGAGGTTATTCTTCCAAAGT 1500 1441 CTAGTCTTTGAGTGTGCAGATTTAGGACAAATGTGGAGGTTATTCTTCCAAAGT 3924 1501 ACGGTTGCTTGAATCTAAGCAATGTCAAGAATCTACAAATGTGGAGGTTTTTCTTGGA 1560 1501 ACGGTTGCTTGAATCTAAGCAATGTCAAGAATCTACAAAATCCATCAAAGTTTTCTTGGG 1560 3925 ACGGTTGCTTGAATCTAAGCAATGTCAAGAATCTACAAAATCCATCAGAGTTTTTCTTGGG 3984	1621 GTGGTTCTGAAATAATGGTGGCGTGGACTAGTCGAAGCCCTTTGTGTTTATTTCTGGG 4144 1621 AACTCGAAATGGATGTTTGGAATTAGTTGGAGCGCTTTGTGTTTTATTTCTTGGG 4144 1045 AACTCGAAATGGGATGTTTGGAATTAGTTCGAAGCGAACTGTTTAGTTCTCCGAAGTGTTTGTT	

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Springer, Franziena
Springer, Franziena
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENTYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
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                                                                                                                                                                                         NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-JUL-1997
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
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46.4%; Score 1204.8;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 1735; Conservative 0; Mismatches
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FILING DATE: 29-Oct-2002
CLASSIFICATION - UNKNOWN-
APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/POCKET NUMBER: Agrevo-4
TELECOMMULCATION INFERMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9000
                                                                                                                                                                                                                                                                                                                                   ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUMTYPE: BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 307..3897
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-284-668-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: DE P 44 41 FILING DATE: 10-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Solanum tuberosum
                                             AL INFORMATION:
APPLICANT: Kossmann, Jens
envinger, Franziska
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Sequence 11, Application US/10284668
Publication No. US20030106100A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA to RNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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STRANDEDNESS: single
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TISSUE TYPE: leaf
                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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Qy 2339 TCTCTCGCATCTGATATACGCTGGCTCTGACTTCTGGTCCCATCTATATTTGAGCC 2398 bb 3516 ACTITCTCACCTGATATATGCTGGTGTTTTATTCTTGATCCTTCAATATTTGAGCC 3575 Qy 2399 TTGCGGCCTAACTCGCTGTGGCGTATGGAACCATCCGGTAGGACCATGCGCTAAGAC 3635 Db 3576 ATGTGGACTTACACTCGTCTTCGATGTGGACATTCCAATTCCAGTCGTGGCTAAAAC 3635 Qy 2459 TGGAGGCTCTTCGACTCTTCGATGTGGACAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCA	RESULT 5 US-10-264-668-1 Sequence 1, Application US/10284668 Sequence 1, Application US/1028468 Publication No. US2030106100A1 GENERAL INFORMATION: APPLICANT: Kossmann, Jens Springer, Franziska Abel, Gernot INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES CORRESPONDENCE ADDRESS: ADDRESSEE: FISH & NEAVE STREET: 1251 Avenue of the Americas CITY: New York START: New York STARTS. New York	RM: oppy disk c compatible The PC-DOS/MS-DOS The Release #1.0, DATA: BER: US/10/284,668 -Oct-2002 -Unknown> TA: UNKnown> TA: UNKNOWN> TA: UNKNOWN> TA: UNL-1997	ATTORNEY GATE: 09-NOV-1995 ATTORNEY AGETICATION NUMBER: PCI EP 44 14 408.0 FILING DATE: 10-NOV-1994 ATTORNEY AGENT INFORMATION: REGISTRATION NUMBER: 27,794 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 212-256-9000 TELEPHONE: 212-556-9000 TELEPHONE: 212-556-9000 TELEPHONE: 212-556-9000 TELEPHONE: 212-556-9000 TELEPHONE: 212-556-9000 TELEPHORE: 212-556-9000 TELEPHONE: 212-566-9000 TELEPHONE: 212-556-9000 TELEPHONE: 212-556-9000 TELEPHONE: 212-566-9000 TELEPHONE: 212-566-9000 TELEPHONE: 212-566-9000 TELEPHONE: 212-566-9000 TELEPHONE: 212-566-9000 TELEPHONE: 212-566-9000 TELEPHONE: 212-566-9000 TELEPHONE: 212-566-90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 3..2033
LOCATION: 10..2033
OTHER INFORMATION: /function= "Polymerization of starch"
/product= "Starch synthase"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Э,
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.8%; Score 931; DB 15; Length 2303; Best Local Similarity 68.5%; Pred. No. 1.1e-268; Matches 1301; Conservative 0; Mismatches 595; Indels 3
                                                                                                                   LIBRARY: cDNA-library in pBluescriptSKII
ORGANISM: Solanum tuberosum
                            STRAIN: cv Berolina
TISSUE TYPE: tuber tissue
                                                                                       IMMEDIATE SOURCE
                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                           US-10-284-668-1
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ζŏ	43 ATCAGAGTTTTTCTTGGGGTGGT	GIGGCGTGGACTAGTCGAAGGCC 16
ΩD		
QY	03 TTTGTGTTTACTTCCTGGAA	AGTCGGATATGTATA
qq	CTATTTTT	TTTCGAAAGGGTGCGTCTATGGTT 972
δλ	60 GCAGGGACGATGACCGCCGA	STICTGCICIAGAGITICICCICC 1719
වි	ragcaargargraacgarttgrift	dedeirriedakirireireis
δy	1720 AAAGTGGATCTTCTCCGAACATAATACATTGCCAT	3GTCAAGTGCTCCTGTTGCCT
qq		ATTGGTCTAGTGCTCTGTTGCTT 1092
λõ	1780 GGCTACACAAGGAAAACTACGCGAAGTCTAGCTTG	183
Dþ	 93 GGCTCTTTAAGGAACAATATA	CACACTATGTCTAAGCAAATCTCGTATAGTCTTCACGA 1152
δλ	40 TCCACAATCTTGAATTTGGAG	189
qq	CATAATCTT	ACTAACGCAGACAAA
٥٧	00 CAACAACTGTCTCTAATACATAT	SGIGCCATAGITCCIC 195
qq	13 CTACAACAGTTTCACCAACTTAC	CTGGAAACCCTGTAATTGCGCCTC 1272
ζŏ	1960 AICTIGGGAAATICTAIGGCAITCTCAAIGGAAIT	CGGATATATGGGATCCGTAC
Dþ	73 ACCTTCACAAGTTCCATG	AGATATTTGGGATCC
δλ	2020 ATGACAACTITAICCCGGTCCACTACACTIGIGAG	GGTTGAAGGCAAGAGGGCTG 207
Db	33 ACGATAAGTTCATTCC	
δλ	ACTG	SATGTCCCCGTCGTAGGAA
DP	393	
δý	CGCCTG	AAGCATGCGATTCACCGTA 219
Ωþ	53 TTATCACCGCTTAACTCACAGAAAGGAATCCAC	
Qy	00 CACTCGAACGGAACGGACAGGTGGTTTTGCTTGGT	AGCGCCGGACTCTCGAATC
qq	13 ccriggaa	
λŏ	2260 CIGATITIGICAACCIGGCGAATACGCTCCACGGC	3AG
qq	73	ATATAATGACGCGCACGACTCT 1632
λõ	2320 CCTTGACCTACGACGAGCCTCTCGCATCTGATA	CATTCTGG 237
qu	1633 GTCTAACATATGACGAGCCACTTTCTCACCTGATATATGC	
ζ	CCAT	CGCCATGCGGTATGGAACCA 24
QQ	93 TTC	
δ'n	TCCCGA	CTTCGATGTGGACAATGACA 24
Db	53	STATITGAIGTIGACCAIGACA 181
δλ	00-	GETTTAGCTTTGACGGAGCTGATA 2559
DÞ	13	rrcagcrtrgarggagca
Οy	2560 GCAACGGTGTTGACTACGCGCTGAACAGGGCGATCT	CAG 2598
Db	73 CTGGCGGAGTTGATTATGCTCTGAATAGAGCTCT	191

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TGACCTACGACGACCTCTCTCGCATCTGATATACGCTGGCTCTGACTTCATTCTGGTCC 2382
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Best Local Similarity 66.4%;
Matches 1411; Conservative
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ORGANISM: Zea mays
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LENGTH: 2581
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                        Sequence 20351, Application US/10425114

Sequence 20351, Application No. US20040034888A1

Bublication No. US2004003488BA1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Pance of Invention Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 1338
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                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: LIB3180-041-All_FLI
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Zea mays FEATURE:
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APPLICANT: 2004, Vibua
APPLICANT: 2004, Vibua
APPLICANT: Screen, Steven B
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53313)B
CURRENT PRILITY OF DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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Pred. No. 3.9e-237;
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US-10-425-114-30909
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zou Yihua
APPLICANT: Zou Yihua
APPLICANT: Zon Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APLICATION NUS: 285684
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US-10-424-599-97896
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ORGANISM: Glycine
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US-10-424-599-97896
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Length 2218;

DB 13;

27.9%; Score 724.4;

Db 1032 AAATGATTTGTGAATTGCCAATGAATTGCATTCCGCTCATCATGATCGTGCTAGAC 1091 Oy 2317 TTTCCTTGACCTACGAGGGCTCTCGCATCTGATATAGCTGGTCTCTATC 2376 1092 TTTGCCTTGATATGATGAGCCTCTTCACATTGATATATGCTGGTGTTCATTC 1151 Oy 2377 TGGTCCATCTATATTTGAGCCTTGCGCCTACTCGCCATGCGGTATGGAA 2436 Db 1152 TAGTTCCTTCATCTTTGAGCTTGCGCCTACTCGACTCGTCGCCATGCGTTTGTT 1211 Oy 2437 CCATCCGATTGTCGCAAAACTGGAGCTCTTCGACACTCTTCGATGTGATA 2496 Db 1212 CAATACCTGTTGTTCGGAAAACTGGAGGATTTTGATCGACATTGATGATG 1271 Oy 2437 CCAACGAAACGAGCGCAAGGGCTTTACGATATTGGAGTTTTGATGACGTTGTTGATGACTTTTGATGAGGTTTTTGATGAGGTTGTTTTTTAGTGAGAGCTGTTTTTAGTGAGAGTTTTTGATGAGGTTGTTTTTTTT	14 9 14 25 14 25 15 26 16 26 16 26 17 26 17 26 17 26 17 26 17 27 17	Ouery Match Query Match Best Local Similarity 76.3%; Score 480.4; DB 13; Length 1181; Best Local Similarity 76.3%; Pred. No. 4e-133; Matches 586; Conservative 0; Mismatches 176; Indels 0; Gaps 0; 1832 ATTCACCACCACATCTTGAATTGGAGGCATCACATGGCAAGGCAATGGCACATG 60 Qy 1892 TGATAAAGCAACATCTTCAATACATTCAAAGGAAATGGCACATTG 60 Qy 1892 TGATAAAGCAACATGTTATCCAATACATTCAAAGGAAGGCAATGGGCCATT 120 Qy 1952 AGTTCCTCATTTATCCATACATACATCGAAAGGAAGGCAATGGGCCAT 1951
Best Local Similarity 71.7%; Pred. No. 1.9e-206; Matches 977; Conservative 0; Mismatches 381; Indels 4; Gaps 2; 1240 TITACGTTCCACGAGATGCCTATATGATGGACTTCCGTTTTCTCGGAGTCAGAAGGTG 1299 13 TIAAGGTTCCACTGATGATGATGATGATTCTTCTCTGAGATGAAGGTG 72 1300 GAATTTATGATAACGAAATGGCTATAATTCTTTTTTTTTT	1540 TCCATCAGAGTTTTCTTGGGGGGGGCTCGAAATAAATGTGGGGGTGGACTAGTCGAAG 1599 112 GTCACATAGGATTTTCTGGGGGGCTGGAATAAAAGTATGGCATGGAAAGTTGTGAGG 371 1600 GCCTTTGTGTTTACTTCCTGGAACTCAAATAGGATTTGGCATGGAAAGTTGGGATTGGGATGTTGGGATTGGGATTGGGATTGGGATTGGGATTGGGATTGGGATTGGGATTGGGATTGGGATTGGGATTGGGATTGGGATTGGGATTGGATTGGTTTGGAAGTTGGTGTATAGGATTGGTTTGTTG	1897 AAGCAACAACTGTCTCTAATACATATTCAAAGGAAGTGTCAGGTCCCTAGTTC 1956

	do Qy	63 CAGITTACTATAATCCGGCCAATACAGTACTTAATGGTAAACCTGAAATTTGGTTCAGAT 122 1150 GITCCITTAATGGTTGGATGTATGCAGGTGTTGCCACCTCAAAGATGGTAGAAG 1209
CTCG 42	qq	
AATCCAAGCTGATTTTGTCAACCTGGCGAATACGCTCCACGGCGTAAACCATGGGCAAGT 2311 	QY	1210 CAGAAAATGGTTCACACCTAAAAGCAACAGTTTACGTTCCACGAGATGCCTATATGATGG 1269
GAGGCITICCITGACCIACGACGACGCICTCGCATCTGATAIACGCTGGCTCTGACTT 2371	Qy du	1270 ACITCGTITICICGGAGTCAGAAGAGGGAATITATGATAACAGAAATGGGTTAGACT 1329
CATICIGGICCCAICTAIAITIGAGCCITGCGGCCTAACICAGCICGICGCCAIGCGGIA 2431	QY Db	1330 AICATAITCCIGITHINGGGICAAITGCAAAGGAACCACCTAIGCACAITGTCCACAITG 1389
TGGAACCATCCCGATTGTCCGCAAGACTGGAGGCTCTTCGACACTGTCTTCGATGTGGA 2491	Qy	1390 CTGTTGAGATGGCACCAATGGCAAAGGTTGGAGGTCTTGGTGATGTTGTCACTAGTCTTT 1449
CAATGACAAGGAACGAGGCCCGAGGCCTTGAGCCCAACGGGTTTAGCTTTGACGG 2551	QV Dp	1450 CACGIGCIGIGCAAGAITIAGGACACAAIGIGGAGGIJAITCITCCAAAGIACGGIIGCI 1509
AGCTGATAGCAACGGTGTTGACTACGCGCTGAACAGGGCGAT 2593	& 43 €	1510 IGAATCTAAGGAATGTCAAGAATCTACAACATCATCAGAGTTTTTCTTGGGGTGGTTCTG 1569
ULT 10 10-341-91 10-341-91	ò q	1570 AAATAANGGGGGGGGGGGCTAGTCGAAGGCCTTTGTGTTA 1612
Publication No. US20040006787A1 GENERAL INFORMATION: APPLICANT: Boyce Thompson Institute for Plant Research, Inc. APPLICANT: Curagen Corporation APPLICANT: Crasts, Oswald APPLICANT: Swirsky, Peter APPLICANT: Mysore, Kiran	RESULT US-09- ; Sequ ; Pate ; GENE ; APP	11 739-438-3 ence 3, Application US/C nt No. USZ0020003394A1 RAL INFORMATION: LICANT: Allen, Steve
APPLICANT: Folkerts, Otto APPLICANT: Martin, Gregory APPLICANT: Martin, Gregory APPLICANT: Martin, Gregory TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOG TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE FILE PEPEPENCE: NTT 6722	APP APP TIT FILL	APPLICANT: Beckles, Diane M. APPLICANT: Thorpe, Cathy TITLE OF INVENTION: Homologs of Starch Synthase DU1 FILE REFRENCE: CHRENT APPLICATION NUMBER: US/09/739, 438 CHRENT FILING DATE: 2000-12-18
E 0 . 0	PRIOR PRIOR NUMBE SOFTW	PRIOR APPLICATION NUMBER: 60/171514 PRIOR FILING DATE: 1999-12-22 NUMBER OF SEQ ID NOS: 6 SOFTWARE Microsoft Office 97
FAILOR PEPLICATION NOMBER: 00261029 PRIOR FILING DATE: 2001-01-11 PRIOR APPLICATION NUMBER: 60348792 PRIOR FILING DATE: 2002-01-14 NUMBER OF SEC 10 NOS: 395	ALL STATE OF THE S	NY 15 3 LENGTH: 548 TYPE: DNA ORGANISM: Oryza sativa
SOFTWARE: Stentin version 3.1 SEQ ID NO 91 LENGTH: 585 TYPE: DNA ORGANISM: Lycopersion esculentum S-10-341-961A-91		NAME/KEY: unsure LOCATION: (312) NAME/KEY: unsure LOCATION: (408) LOCATION: (548)
atch 12.2%; Score 315.8; DB 16; Length 585; cal Similarity 71.4%; Pred. No. 9.4e-84; 416; Conservative 0; Mismatches 167; Indels 0; Gaps 0; 1030 TITCICAGABACACATGITTACACCGAACCACTGAAATACACCTGGAACTACTATTG 1089 13 TITCICAGAACAAGAACAACTATAAATACTAAAATACTAAAACAACAGAACAACAACAACAACAACAACAACAACAAC	US-09- Quer Best Mato	
	ΩD	3 CAGCAATGACGAGAGTAGATTTGGCTTCTTCTGCCATTCTGCTCTAGAGTTTCTCGGCCA 62

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2311 TGAGGCTTTCCTTGACCTGCGAGCCTCTCTCGCATCTGATATACGCTGGCTCTGACT 2370
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181 GATTTGGTTTTTTTTTTGTCATGCTGCTCTTGAATTTCTACATCAAAATGGATTTCATCCGG 240
                                                                                                                       241 ATGTCATCCACTGCCATGATTGGTCGAGTGCGCCAGTTGCATGGCTATCTAAAGAACAGT 300
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                                                                          1738 ACATAATACATTGCCATGATTGGTCAAGTGCTCCTGTTGCCTGGCTACACAAGGAAAACT
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Patent No. US2002029394A1
FATENT INFORMATION:
APPLICANT: Backles Diane M.
APPLICANT: Thorpe, Cathy
TITLE REPRENCE:
CURRENT APPLICATION NUMBER: US/09/739,438
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/171514
PRIOR APPLICATION NUMBER: 60/171514
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Microsoft Office 97
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Best Local Similarity 72.3
Matches 295; Conservative
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ORGANISM: Oryza sativa
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LOCATION: (372)
NAME/KEY: unsure
LOCATION: (404)
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APPLICANT: La Rosa Thomas J
APPLICANT: Exou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Sono Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 83485
LENGTH: 641
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                                                                                                                                                                                                 CCACAATCTTGAATTTGGAGCGCATCATATTGGCAAAGCAATGAGATATTGTGATAAAGC 1900
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                                                63 AAATGGATCTTCTCCTGATATTATACATTGTCATGATTGGTCAAGTGCTCCAGTTGCTTG 122
                                                                                                                                                 123 GCTATTCAAGGAACAATATGCTCAAAATGGACTGTCAAATGGGCGGGGTTGTATTTACCAT 182
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       1721 AAGTGGATCTTCTCCGAACATAATACATTGCCATGATTGGTCAAGTGCTCCTGTTGCCTG
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10.9%; Score 283.8; DB 13; Length 641;
Best Local Similarity 66.1%; Pred. No. 4.4e-74;
Matches 424; Conservative 0; Mismatches 214; Indels 3;
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LOCATION: (1)..(641)
OTHER INFORMATION: unsure at all n locations
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Publication No. US20040031072A1
GENERAL INFORMATION:
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US-10-424-599-83485
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APPLICANT:
APPLICANT:
APPLICANT: Ico, Leuran, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
TITLE REPREMENC: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: April 21, 1998
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OTHER INFORMATION: Incyte ID No. US20010051335A1 700379870H1

NAME/KEY: unsure

LOCATION: 2, 56, 78, 121, 125, 187-188, 197, 270

STHER INFORMATION: a, t, c, g, or other
US-09-294-093B-3346
                        762
                                                                        422 GTTCTAAAAAGAGGTGAATGGTGGTATGCTGATGTTGTTATAC 464
                          720 CATGACAAAGATTGTGATTGGTGGTTTGCAGATGTTGTCGTGC
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Job time : 1501 secs
                                                                                                                                                                                                      Sequence 3346, Application US/09294093B Patent No. US20010051335A1
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APPLICANT: Lal
                                                                                                                                                   RESULT 15
US-09-294-093B-3346
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LENGTH: 297
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREBENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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122 TAAAGCTTTGTTTAACCTATGATGAGCCACTATCTCATTTGATTTATGCTGGTGCCGACT 181
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US-10-424-599-84418
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Publication No. US20040031072A1
GENERAL INFORMATION:
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: June 20, 2004, 05:01:30 ; Search time 9811 Seconds (without alignments) 7907.649 Million cell updates/sec	Title: VS-10-634-262-1_COPY_2425_5022 Perfect score: 2598 Sequence: 1 agcttgctgaaaaaattatgctgaacaggcgatctcag 2598	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 27513289 segs, 14931090276 residues	Total number of hits satisfying chosen parameters: 55026578	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Fost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : EST:* 1: em_estba:* 2: em_estbum:* 3: em_estin:*	# # # # # # # # # # # # # # # # # # #	o: em_estro:* 8: em_htc:*	9: gb_est1:* 10: gb_est2:* 11: gb_est2:*	12: gb_est3:* 13: gb_est4:*	14: gp_estb:* 15: em_estfun:* 16: em_estcon:*	17: em_ges_hum:* 18: em_ges_lnv:* 19: em_ges_pln:*	e e		55		thar thar	SUMMARIES	ery tch Length DB ID Descripti	1 2468.2 95.0 6030 11 AY110586 AY110586 Zea mays 2 771.4 29.7 971 14 CD437215 CD437215 EL01N0370 3 746.4 28.7 773 14 CA404552 CA404552 EL01N0519 4 731.6 28.2 751 14 CD445384 CD445384 EL01N0450

26.3 26.3 26.3 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	Spermatophyta; magnollophyta; Lillopsicaled; Panicoideae; Andropogoneae; Zea I a (bases 1 to 6030) arine, Miao, G.H., Voge; Arthur, L.W., Hanafey, M., Morgante, M. an Maize Mapping Project/DuPont Consensus Thombished (2002)	HTC. Zea mays Zea mays Eukaryota; Viridiplantae; Streptophyta; E Spermatophyta; Magnoliophyta; Liliopsida; clade; Panicoideae; Andropogoneae; Zea.		ALIGNMENTS	3.1 545 1 2.6 555 9 2.6 531 1	3.4 690 1 3.1 545 1	3.8 680 1	4,0 548 1 3.9 536 1	4.4 560 1 4.2 627 1	4.4 556 1	4.6 827 1 4.5 822 2	5.0 805 1	5.9 622 1	5.9 602 1	6.1 804 1	5.6 441 1.5.3 709 13	5.8 782 I.	5.9 646 1.	5.9 662 21	7.6 610 9	7.7 466 1-	3.1 638 28	831 12	5.0	5.3 705 14 5.1 692 14	
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                                                                                                                               /note-"this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuFont contigs; this resource was assembled by DuFont as part of a collaboration for the covergo addressing of BACs in conjunction with the Maize Mapping Project"
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maize cDNA sequences is either Virginia Walbot, Stanford or E
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
                                                     /organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:630603"
/db_xref="taxon:4577"
/clone lib="Maize Mapping Project/DuPont Cornsensus Library"
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841	GACATGATTITCATGCTACCCTTCCAAATAACATGACTGACGAAGAAGATTCGATGGAAG 900	
7 7	caarggatctatacaaggcttcaacaagagaggaggaaaagggaggaggctatta 	
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1081	CIATTGAIGTGCITTATAATCCITCTAATACAGTICTAACTGGAAAGCCAGAGGTIT 	
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1261 3685	ATATGATGGACTTCGTTTTCTCGGAGTCAGAAGGAGGTGGAATTTATGATAACAGAAATG 13	
1321	GGTTAGACTATCATATTCCTGTTTTTGGGTCAATTGCAAAGGAACCACCTATGCACATTG 138 	
	TCCACATIGCTGTIGAGATGGCACCAATCGCAAAGGTTGGAGGTCTTGGTGATGTTGTCA 144	
1441	CTAGTCTITCACGTGCTGCAAGATTTAGGACACAATGTGGAGGTTATTCTTCCAAAGT 15	
1501	ACGGTTGCTTGAATCTAAGGAATGTCAAGAATCTACAAATCCATCAGAGTTTTTGTTGGG 156	
561 985	GIGGITCIGAAAIAAAIGIGIGGCGIGGACIAGICGAAGGCCTIIGIGIIIIACITCCUGG 	
2 4	AACCTCAAAATGGGATGTTTGGAGTGGAATATGTATATGGCAGGAAGGA	
1681	TIGGCTICTICTGTCGTTCTGCTCTAGAGTTTCTCCTCCAAAGTGGATCTTCTCCGAACA 174	
1741	TAATACATIGCCATGATIGGTCAAGIGCTCCTGTIGCCTGGCTACACGAAAACTACG 	
1801	TITGGCAAACGCACGGGTGGTATITCACCATCCACAATCITGAATTIGGAG 	

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Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlaiowaksman.rutgers.edu
Seq primer: T7
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Best Local Similarity 99.2%;
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                                   4285 CGCATCATATTGGCAAAGCAATGAGATATTGTGATAAAGCAACAACTGTCTCTAATACAT
                                                         ATTCAAAGGAAGTGTCAGGTCATGGTGCCATAGTTCCTCATCTTGGGAAATTCTATGGCA
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Unpublished (2002)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
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Lai,J., Dey,N., Kim,C.S.,
Messing,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 ATTGATGICCCCGTCGTAGGAATCGTCACTCGCCTGACAGCCCAAAAGGGGATCCACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGGATATATGGGATCCGTACAATGACAACTTTATCCCGGTCCACTACACTTGTGAGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2118 ATCGATCTCCCCGTCGTAGGAATCGTCACTCGCCTGACAGCCCCAAAAGGGGATCCACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAATGAGATATTGTGATAAAGCCACAACTGTCTCTAATACATATTCAAAGGAAGTGTCTC
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                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                              /organism="Zea mays"
/mol type="mxNX"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_3"
/note="Vector: pBluescript SK-; Site_1: ECORI; & Xhol"
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0
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1561 GTGGTICTGAAATAAATGTGTGGCGTGGACTAGTCGAAGGCCTTTGTGTTTTACTTCCTGG 1620
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                    AGGCAAGAGGGGCTGCTAAGAGGGCACTGCAGCAGAAGTTTGGGTTACAGCAAATTGATGT 497
378 AIGGGAICCGIACAAIGACAACITIAICCCGGICCACIACACTIGIGAGAAIGIGGIIGA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol type="mra"
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/db xref="taxon:4577"
/tissue type="Endosperm of 7-23DAP"
/clone lib="Endosperm 4"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: xhoI"
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                                                                                                       CCCCGTCGTAGGAATCGTCACTCGCCTGACAGCCCAAAAGGGGGATCCACCTGATCAAGCA
                                                                                                                                                                                                            558 IGCGATTCACCGTACACTCGAACGGAACGGACAGGTGTTTTGCTTGGTTCAGCGCCGGA
                                                                                                                                                                                                                                                                                                                       GCAAGTGAGGCTTTCCTTGACCTACGACGAGCCTCTCGCATCTGATATACGCTGGCTC
                                                                                                                                         498 ccccorcoradoarcorcacroscordacadoccaaaadogoarcoaccroarcaada
                                                                                                                                                                              TGCGATTCACCGTACACTCGAACGGACAGGTGGTTTTGCTTGGTTCAGCGCCCGGA
                                     AGGCAAGAGGGCTGCTAAGAGGGCACTGCAGAAGTTTGGGTTACAGCAAATCGATGT
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Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E.
Messing,J.
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EL01N0450H08.b Endosperm_4 Zea mays cDNA, mRNA sequence.
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Pred. No. 2.3e-179;
0; Mismatches 9;
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Unpublished (2002)
Ontact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 088
Tel: 732-445-5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: jlai@waksman.rutgers.edu
Seq primer: T3.
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/organism="Zea mays"
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CD445384
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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/organism="Zea mays"
/organism="Zea mays"
/oultiva="W22"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib=Endosperm 4"
/note="Vector: pBluesGript SK-; Site_1: EcoRI; Site_2:
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Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E.
Messing,J.
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Pred. No. 3.2e-183;
0; Mismatches 6; Indels 0:
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                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Contact: Lai, Jinsheng
Contact: Lai, Jinsheng
Wakeman Institute, Ruggars University
190 Frelinghuysen Rd., Piscataway, NJ 081
Tel: 732-445-3801
Email: jlai@wakeman.rutgers.edu
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Best Local Similarity 99.2%;
Matches 750; Conservative (
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/tissue type="Endosperm 4"
/clone lib="Endosperm 4"
/note="Vector: pBluesGript SK-; Site_1: EcoRI; Site_2: Xhol"
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                                                                                                                                                                                                                                                                          8 GGGSTTATTCTTCCAAAGTACGGTTGCTTGAATCTAAGGAATGTCAAGAATCTACACATC
                                                                                                                                                                                                                                                                                                             CATCAGAGITITITICITGGGGTGGTTCTGAAATAAATGTGTGGGCGTGGACTAGTCGAAGGC
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EL01N0320B09.b Endosperm_3 Zea mays cDNA, mRNA sequence.
CD434207
CD434207.1 GI:31349850
EST.
Zea mays
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26.3%; Score 683.6; DB 14;
Best Local Similarity 98.7%; Pred. No. 7.4e-167;
Matches 689; Conservative 0; Mismatches 9;
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1 (bases 1 to 705)
Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and Messing,J.
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                                                                                                                  TIGGCTICTICTGTCGTTCTGCTCTAGAGTTTCTCCTCCAAAGTGGATCTTCTCCGAACA
                                                                                                                                    1741 TAATACATTGCCATGATTGGTCAAGTGCTCCTGTTGCCTGGCTACACAAAAATTACG
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                                                                                                                                                                                                                                                                                                                                                                                      426 ATTCAAAGGAAGTGTCAGGTGCCATCGTTCCTCATCTTGGGAAATTCTATGGCA
                                                                           Wakeman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, I
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing of the maize endosperm ESTs
Unpublished (2002)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
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Caixa Postal 6010, 13083-970, Camy
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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/db_xref="taxon:4547"
/clone="SCAGSB1089G09"
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Matches 551; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol type="mRNA"
/cultivar="W2"
/dubxref="waxon:4577"
/tissue type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_3"
/none="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: Xho!"
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Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
Messing,J.
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Pred. No. 2.7e-165;
0; Mismatches 9; Indels 0;
                                                                                                                                                                                   Unpullished (2002)
Unpullished (2002)
Contract: Lai, Ulmsheng
Dr. Joachim Messing's lab
Dr. Joachim Messing's lab
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
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                                                                                                                                                       Sequencing of the maize endosperm ESTs
                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: T3.
Location/Qualifiers
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98.7%;
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/lab host="DBL08"
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/clone library generated from [Stalk Bark from adult cDNA library generated from [Stalk Bark from adult cDNA library generated from polyA+ mRNA using plants] cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose double-strand cDNAs were fractionated in a sepharose class double-strand cDNAs was fragments sizing between 0.8 mid class become of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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Sukaryora, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
   664
                                                        601 ATTGTATTATAACTTAAAGTCTATTCACAGTACTGAAGATATGATGTGATATGATGTGATGG 660
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Pred. No. 3.38-125;
0; Mismatches 27; Indels 1;
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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clone distribution: clone distribution information ca
through the Brazilian clone Collection Center (BCCC)
http://www.bccenter.fcav.unesp.br
Plate: 089 row: G column: 09
Seg primer: T? Promoter Primer.
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TCTTGGGGTGGTTCTGAAATAAATGTGGGGGGGGGCTAAGTCGAAGGCCTTTGTGTTTAAC

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                                                              TTCCTGGAACCTCAAAATGGGATGTTTGGAGTCGGATATGTAATATGGCAGGGACGATGAC 1673
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463 TCTTGGGGTGGTTCTGAATAAATGTGTGGCGTGGACTAGTCGAAGGCCTTTGTGTTTAC 404
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Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,B. and
Messing,J.
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/clone lib="Endosperm 3"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1914 AAIACATATTCAAAGGAAGTGTCAGGTCCATGGTGCCATAGTTCCTCATCTTGGGAAATTC
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                                                                                                                                                                                                                                                                                                                                  283 CCGAACATAATACATTGCCATGATTGGTCAAGTGCTCCTGTTGCCTGGCTACACAAGGAA
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Contact: Lai, dinsheng
Contact: Lai, dinsheng
Waksman Institute, Rutgers University
190 Frealinghuysen Rd., Piscataway, NJ 08854, I Pax: 732-445-3801
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TATGAGAATGTTCCTGGTTTCTCAGAAACACATTGTTTACACCGAACCACTTGAAATACA 1072
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Genoplante
Genoplante
Genoplante
Genoplante
John Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
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cDNA clone QCM33a07, mRNA sequence.
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99.6%; Pred. No. 3.6e-124;
iive 0; Mismatches 2;
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Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Enkaryota; Viridiplantae; Streptophyta; Enkaryota; Poades; Poaceae; PACCAD Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidaea; Andropogoneae; Zea.

1 (bases 1 to 831)

2 (Sprods, J. A. Singh, J. A., Piche, C., Cass, L., Couroux, P., De Simmonds, J. A., Hartis, L.J., Hattori, J. I., Ouellet, T., Robert, L. Sprott, D. and Tinker, N. A.

Expressed Sequence Tags from Cold-Stressed Maize Seedlings Grown Under High Light Intensity
Unpublished (201)
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Zm03_06d02_A Zm03_AAFC_ECORC_cold_stressed_maize_seedlings Zea mays
cDNA_clone_Zm03_06d02, mRNA_sequence.
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                                                                   GAACCACCTATGGACATTGTCCACATTG-CTGTTGAGATGGCACCAATCGCAAAGGTTGG 1420
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1362 ATTTATGATAACAGAAATGGGTTAGACTATCATATTCCTGTTTTTGGGTCAATTGCAAAG 1361
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KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KlA
                                   09
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                                 <u>airiraidaraacadaardoorracacrarcararricciorririroogorcaard</u>
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Eastern Cereal and Oilseed Research Centre
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Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
Location/Qualifiers
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/mol_type="mRNA"

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EST731566 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POCAX21 5' end, mRNA sequence.
CK247929
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Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Solanaceae; Solanum.
1 (bases 1 to 1014)
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                     19.9%; Score 517.4; DB 12; larity 98.5%; Pred. No. 1.8e-123; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CK247929.1 GI:39797565
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CK247929
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265 TTAACGGACACACGGTATATGAAATAATAACAATAATGATTTCGTGATACAATAGAAA 324
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                                                                                                                                                          2105 TGGGTTACAGCAATCGATGTCCCCGTCGTAGGAATCGTCACTGGCTTGACAGCCCGAAAA 2164
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                                                                                                                                                                                                                                                                                                                         TTGCTTGGTTCAGCGCCGGACTCTCGAATCCAAGCTGA-TTTTGTCAACCTGGCGAATA 2283
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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                                                                              2104
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                                                                                                                  721 CÁCCTCAGÁAAACGTTGTTGAAGGCAAACAGCAGCCÁAGGAAGCTTTGCAGGGAAACT
                                                                                                                                                                                                                                          2165 GGGGATCCACCTGATCAAGCATGCGGATTCACCGTACACTCGAACGGAACGGACAGGTGGT
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1985 CAATGGAATTGATCCGGATATATGGGATCCGTACAATGACAACTTTATCCCGGTCCACTA
                                 661 GAATGGGATTGACCCAGATATTTGGGATCCTTTAAACGATAAGTTCATTCCGATTCCATA
                                                                              CACTIONGAGAATGTGGGTTGAAGGCAAAGAGGCTGCTAAGAGGGCACTGCAGCAGATT
                                                                                                                                                                                                                                                                                                                                                                                                         2284 CGCTCCACCGCTAAACCATGGGCAAGTGAGGCTTTCCTTGACCTACGACGAGC 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                               961 AATIGCACTCCAAATATAATGACCGCCACGACTCTGTCTAACATATGACGAGC 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BZ970127 638 bp DNA linear GSS 25-M
PUGGN91TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa379013,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 638)
whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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/clone="ZMMBTa379013"
/clone=lb="ZM-06-1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: lcor selected genomic DNA library"
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Best Local Similarity 97.2%; Pred. No. 2.6e-111;
Matches 479; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville, MD
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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/mol_type="genomic DNA"
/strain="B73"
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Class: sheared ends.
Location/Qualifiers
1. .638
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Unpublished (2003)
Other_GSSs: PUGGM91TB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence BZ970127
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                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4113"
/clone="POCAX21"
/tissue_type="callus"
/lab_host="DH10B-TonA"
/clone_lib="potato_callus_cDNA_library, normalized_and_full-length"
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                       Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from potato callus tissue Unpublished (2003)
Contact: Robin Buell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.8%; Score 488.4; DB 14; Length 1014;
ilarity 68.9%; Pred. No. 7.1e-116;
Conservative 0; Mismatches 311; Indels 4;
                                                                                                         The Institute for Genomic Research 712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@tigr.org Clones can be requested from TIGR via potato@tigr.org Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                   /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
                                                                                                                                                                                                                                    1014
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Best Local Similarity
Matches 699; Conserv
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Email: fgas ests@cs.usask.ca
This sequence is the direct result of the Base calling software
This sequence is the direct result of the raw base calls. To aid in the
phred (default parameters). It is the raw base calls. To aid in the
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identification of the high quality insert the software Lucy
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Triticum aestivum
Triticum aestivum
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Triticum aestivum
Triticum aestivum
Sukaryota; Viridhjaliatae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases; Troiticeae; Triticum.
1 (bases; Troity, Danyluk, J., Budes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Iaroche, A.,
Ininks, M.G., Mocrathy, E.L., Monroy, A., Muzak, I., Nilson, D.,
Penniket, C., Roach, J.L., and Sanhan, F.
Functional, Annois of Abiotic Stress In Wheat and Canola Crops
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                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGACCTCTAGTTCACAGTACTGAGATAGGATGCATGGTGGCTATAACAATTGGATTG
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                                                                                                                                                                                                                                                                                                                                                                                  338 ACATTGAGCCCATCACGACTGGACAAGAGGCTACTGTCAGATTGTATTATAACATAAACT
                          505 AGAAGAATAAATTGTGCAATGTATTGGGTTTAGCCAGAGCTCCTGTTGATATTTATGGT
                                                                                                                                                                                                                                                                                               398 AGAAGAATAAATTGTGCGAATGTATTGGGTTTAGCCAGAGCTCCTGTTGATAATTTAAGGT
GCACCATGGATGAAATTTATTTGAGGATTTCTTGGCTGAAGAAAAGCAACGAGAACTTG
                                                                                   AGAACCTTGCAAATGAGGAAGCTGAAAGGAGGAGACAAACTGATGAGCAGCGGCGAATGG
                                                                                                                    AGGAAGAAAAGGCCCCCAGATAAAGCTGACAGGGTACAAGCCAAGGTTGAGGTAGAACAA
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the region [16,824].
Plate: L5B009 row: I column: 20.
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/note="Vector: pCMV.SPORT6; Crown and developmental stages of spike formation in wheat cultivar Norstar. 4 mRNA populations were combined before constructing the library. The first mRNA population is from lcm crown sections after 30 days of cold acclimation. The second is from lcm crown sections after the third instant was a deacclimation (before deacclimation plants were fully vernalized for 49 days). The third is from different developmental stages of spike formation (5 to 50mm) that still have not emerged from the developmental stages of spike and seed formation after having emerged from the leaf (visible). First strand synthesis in this library was done in the presence of methylated dGTP thereby protecting from internal cleavage with NotI."

547 716 ICATCATGACAAAGAITGIGATTGGTGGITTGCAGATGTTGTCGTGCCTGAAAGAACATA 775 668 ATCIGAAGAACAGGAIGGIGATIGGIGGIAAIGCAAAIGTIACTCTACCTGAAAGGGCGCATT 727 535 487 655 607 667 Ä 475 CTTGGCTCAAGAAAAGCAACGAGAACTTGAAACCTTGCAAATGAGGAAGCTGAAAGGAG 415 427 116 TGAGCCTGATGTACTTATCAAAGGAGCATTCAATGGGTGGAAGTGGAGATTTTTCACTGA 175 235 187 gcadecaracadarradacrrrrgrerrrrraardergacacrercrardaaaacaacad 247 TIATAAAGATTICGICCIGCATATAGAAGGTGACGGGGATGAACACTCATTTGAGGACTT 307 127 67 776 IGTATTGGACTGGGTTTTTGCTGACGGCCCACCAGGGAGTGCAAGGAATTATGACAAAA GAGACAAACTGATGAGCAGCAGTGAATGGAGGAAGAAAAGGGCCGCAGATAAAGCTGACAG <u>rigogitcigaritoriataratagategagaetegagaetaaagaraaaaaragarrig</u> 608 dridchiddadhachrhachdandachdaiddachtriandridhadhadhad AGCCAGAGCTCCTGTTGATAATTTATGGTACATTGAGCCCATCACGACTGGACAAGAGGC TACTGTCAGATTGTATTATAACATAAACTCCAAGACCTCTAGTTCACAGTACTGAGATATG GATGCATGGTGACTATAACAATTGGATTGAATGGACTCTTTTGCTGAAAGGCTTGTTCA GGTACAAGCCAAGGTTGAGGTAGAGGACGAAGAATAAATTGTGCAATGTATTGGGTTT 428 GGCACAGGCAAAAGCTGAGGTTGAGACGAGGAATAAATTGCAGCATGTGTTGGGTTT 68 AAGGGGGAGGATGCTTATCAAAGGGGCATTCAATGGTTGGAGATGGAACCATTTCACTGA AAAATTGCACAAGAGCGAGCTGGCAGGGGACTGGTGGTGCTGCAAACTATACATTCCTAA GCAGGCATACAGAATGGACTTTGTGTTTTTTAACGGACACACGGTATATGAAAATAATAA 56 ATTGAAAGCTGATTCAACAATTGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCAA .. H DB 14; Length 1042; Indels Score 463.6; DB 14; Pred. No. 2.1e-109; 0; Mismatches 264; tch 17.8%; al Similarity 70.5%; 633; Conservative (Best Local Similarity 548 296 959 488 536 176 248 416 476 ω 128 236 188 296 356 308 Query Match Matches g à 유 g à g ਨੋ g d ð 엄 ò ò ð d g ð g

728 gergiadagaktrigegiartragergarteaetreggaregeaageaageargiaraaaca 787

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2494 ATGACAAGGAACGAGGCCCGAGATCGAGGCCTTGAGCCCAACGGGTTTAGCTTTGACGGAG
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/mol_type="mRNA"
/ultivat="F2"
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/clone_lib="QCH"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 791)
Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
Messing, J.
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| /organism="Zea mays" |
|/organism="Zea mays" |
|/organism="Yee="RNA" |
|/oultivat="W22" |
|/db_xref="taxon:4577" |
|/tissue type="Rndosperm of 7-23DAP" |
|/clone lib="Endosperm 3" |
|/ore="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI" |
                                                                      2194 ACCGTACACTCGAACGGAACGGACAGGTGGTTTTGCTTGGTTCAGCGCCGGACTCTCGAA
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99.6%; Pred. No. 5.6e-109;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                              Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ
Tel: 732-445-3801
                                                                                                                                                                                                                                                                                                                         Sequencing of the maize endosperm ESTs Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.
Location/Qualifiers
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QCH1a11.yg QCH Zea mays cDNA clone QCH1a11, mRNA sequence.
CF038283
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
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                                                                                              2598
                                                                                                                       93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                            2554 CTGATAGCAACGGTGTTGACTACGCGCTGAACAGGGCGATCTCAG
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17.7%; Score 459; DB 14; L
Best Local Similarity 100.0%; Pred. No. 2.5e-108;
Matches 459; Conservative 0; Mismatches 0;
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Search completed: June 20, 2004, 12:51:09 Job time: 9817 secs

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